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Minimum
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seq length: 2000000000
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24791104 seqs, 12571243825 residues
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                              Cgn2_6/ptodata/1/pna/US08_COMB.seq:*
(Cgn2_6/ptodata/1/pna/US08_COMB.seq:*
(Cgn2_6/ptodata/1/pna/US092_COMB.seq:*
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(Cgn2_6/ptodata/1/pna/US092_COMB.seq:*
(Cgn2_6/ptodata/1/pna/US093A_COMB.seq:*
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(Cgn2_6/ptodata/1/pna/US095B_COMB.seq:*
(Cgn2_6/ptodata/1/pna/US097B_COMB.seq:*

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44: /cgn2_6/ptodata/1/pna/US6000_COMB.seq:  
45: /cgn2_6/ptodata/1/pna/US6002_COMB.seq:  
46: /cgn2_6/ptodata/1/pna/US6002_COMB.seq:  
47: /cgn2_6/ptodata/1/pna/US6002_COMB.seq:  
48: /cgn2_6/ptodata/1/pna/US6005_COMB.seq:  
49: /cgn2_6/ptodata/1/pna/US6005_COMB.seq:  
50: /cgn2_6/ptodata/1/pna/US6006_COMB.seq:  
51: /cgn2_6/ptodata/1/pna/US6006_COMB.seq:  
52: /cgn2_6/ptodata/1/pna/US6006_COMB.seq:  
53: /cgn2_6/ptodata/1/pna/US6000_COMB.seq:  
54: /cgn2_6/ptodata/1/pna/US6010_COMB.seq:  
55: /cgn2_6/ptodata/1/pna/US6011_COMB.seq:  
56: /cgn2_6/ptodata/1/pna/US6011_COMB.seq:  
57: /cgn2_6/ptodata/1/pna/US6011_COMB.seq:  
58: /cgn2_6/ptodata/1/pna/US6011_COMB.seq:  
59: /cgn2_6/ptodata/1/pna/US6011_COMB.seq:  
60: /cgn2_6/ptodata/1/pna/US6012_COMB.seq:  
60: /cgn2_6/ptodata/1/pna/US6013_COMB.seq:  
60: /cgn2_6/ptodata/1
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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29 29	29 29	29 29	29	29	29	29	29	29	29	29	29	402	402	402	402	Score
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$\frac{3}{3}$	33 64	25 27	64	32	32	22	$\frac{\omega}{\omega}$	64	32	ယ	33	64	32	27	25	DB
US-09-873-402A-41873 US-09-865-419A-51912	US-09-865-419A-15731 US-60-208-063-2535	US-09-654-617-451847 US-09-684-016-451847	US-60-202-213-1089 US-60-207-458-54563	US-09-850-147-1092	60-	US-09-565-306-82924	US-09-865-439A-18142	US-60-202-213-10	US-09-850-147-10	US-09-865-439A-4361	US-09-865-439A-8889	US-60-202-213-1	US-09-850-147-1	US-09-684-016-457554	US-09-654-617-457554	ID
Sequence 41873, A Sequence 51912, A	Sequence 15731, A Sequence 2535, Ap	Sequence 451847, Sequence 451847,	Sequence 1089, Ap Sequence 54563, A	Sequence 1092, Ap	40,	Sequence 82924, A	Sequence 18142, A		Sequence 10, Appl	Sequence 4361, Ap	Sequence 8889, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 457554,	Sequence 457554,	Description

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APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong Annotated Plant Ge
TITLE OF INVENTION: 38-21(15097)D
CURRENT APPLICATION NUMBER: US/09/654,617
CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 463173
SEQ ID NO 457554
LENGTH: 402
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Sorghum bicolor US-09-654-617-457554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1.54-617-457554
US-09-654-617-457554; Sequence 457554, Application US/09654617; GENERAL INFORMATION:
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Best Local S
Matches 402
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Local Similarity 100.0%;
les 402; Conservative (
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 CCTTGAACTTGTGTGGTCTGCACCCTAATTATTGCTCAGATGTGGCAATGGAGCTTCTAT
                                                           AATTTTAGAAGGCAATATTTAAATCTGGAAGGGGTAAAGAACAATCAGATGGTGTTAATT
                                                                        AATTTTAGAAGGCAATATTTAAATCTGGAAGGGGTAAAGAACAATCAGATGGTGTTAATT
                                                                                                                               ACAACCAGATTCCAGGGCCAAGGGCTTGGAATCCCATATTTCCTTTGACTTCAGGTGGAC
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US-09-865-439A-116358
US-09-865-439A-93607
US-09-865-439A-93607
US-09-861-478-52
US-09-861-478-52
US-09-861-478-52
US-09-861-478-52
US-09-861-478-52
US-10-219-999-18314
US-10-219-999-18314
US-09-654-617-262628
US-09-654-617-262628
US-09-654-617-262628
US-09-7458-43952
US-09-7458-43952
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US-09-7458-43952
US-09-7458-43952
US-09-744-4000A-14941
US-09-521-640-156054
US-09-521-640-156054
US-09-521-640-156054
US-09-521-640-136054
US-09-630-346-335
US-09-630-346-335
US-09-874-708A-77966
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Pred. No. 2.9e-212;
0; Mismatches 0;
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116358, A

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10004, Ap
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Annotated Plant Get
FILE REFERENCE:
GURRENT APPLICATION NUMBER: US/09/684,016
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/654,617
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS:
SEQ ID NO 457554
LENGTH: 402
TYPE: DNA
ORGANISM: Sorghum bicolor
US-09-684-016-457554
Sequence 1. Application US/09850147
GENERAL IMFORMATION:
APPLICANT: Andersen, Scott E.
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: Nucleic Acid Molecules And
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51914)B
CURRENT APPLICATION NUMBER: US/09/850,147
CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: US 60/202,213
PRIOR APPLICATION NUMBER: US 69/854,617
PRIOR APPLICATION NUMBER: US 09/654,617
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TITLE OF INVENTION:
FILE REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 100.0%; Score 402; DB 27; al Similarity 100.0%; Pred. No. 2.9e-212; 402; Conservative 0; Mismatches 0;
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                                                                                                                  Other Molecules Associated
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; TYPE: DNA
; ORGANISM: Sorghum bicolor
; OTHER INFORMATION: Clone ID: LIB3476-001-Q6-K1-A3
US-60-202-213-1
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                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 09/684,016
PRIOR FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 18014
SEQ ID NO 1
                                                                                                                  Query Match
Best Local Similarity
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Best Local Simi
Matches 402;
                                                                                                       Matches 402;
                                                                                                                                                                                                                                                                                  APPLICANT: Edgerton, Michael
TITLE OF INVENTION: NUCL
TITLE OF INVENTION: PLANTS
                                                                                                                                                                                                                                              FILE REFERENCE: 38-21(51914)A
CURRENT APPLICATION NUMBER: US/60/202,213
CURRENT FILING DATE: 2000-05-08
                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Sorghum bicolor
OTHER INFORMATION: Clone ID: LIB3476-001-Q6-K1-A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 402
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                                                                1 CCGGGCCGGGCTCACCAGCTGGCCCAGTGAAAGGCTTAAAGACATGTGCCAGGAGAAGGGG
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CCTTGAACTTGTGTGTGGTCTGCACCCTAATTATTGCTCAGATGTGGCAATGGAGCTTCTAT 120
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                                                   CCGGGCCGGGCTCACCAGCTGGCCCAGTGAAGGCTTAAAGACATGTGCCAGGAGAAGGGG 60
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                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                          Andersen, Scott E.
                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                  NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
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                                                                                                                  Score 402; DB 64;
Pred. No. 2.9e-212;
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Pred. No. 2.9e-212;
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APPLICANT: Hardeman, Kristine J.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules And
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51936)B
CURRENT APPLICATION NUMBER: US/09/865,439A
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 60/207,458
PRIOR APPLICATION NUMBER: US 60/207,458
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 119126
SEQ ID NO 8889
LENGTH: 341
                                                                                                                                                                                                                                                                                                     RESULT 6
US-09-865-439A-4361/c
; Sequence 4361, Application US/09865439A
; GENERAL INFORMATION:
Michael D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: LIB3205-106-P1-N1-B3 US-09-865-439A-8889
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SEQ ID NO 4361
LENGTH: 351
TYPE: DNA
ORGANISM: Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                   CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 60/207,458
PRIOR FILING DATE: 2000-05-30
                                                                                                                                                                   TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With TITLE OF INVENTION: Plants FILE REFERENCE: 38-21(51936)B CURRENT APPLICATION NUMBER: US/09/865,439A
                                                                                                                                                                                                                                                       APPLICANT: Edgerton, Michael D
APPLICANT: Hardeman, Kristine J.
APPLICANT: La Rosa, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Edgerton, Michael D
APPLICANT: Hardeman, Kristine J.
                                                                                        NUMBER OF SEQ ID NOS: 119126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 AGCTTCTATATTAAGCTTCGATGAGAAGA 140
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  Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.2%; ilarity 100.0%; Conservative
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Pred. No.
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0.00015;
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US-60-202-213-10
Sequence 10, Application US/60202213
GENERAL INFORMATION:
 В
                               QY
                                                                                                                               ; ORGANISM: Sorghum bicolor ; OTHER INFORMATION: Clone ID: US-60-202-213-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORANISM: Sorghum bicolor
; OTHER INFORMATION: Clone ID:
US-09-850-147-10
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US-09-850-147-10
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                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SEQ ID NO 10
LENGTH: 385
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GENERAL INFORMATION:
APPLICANT: Andersen, Scott E.
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: Moleculeic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51914)B
FILE REFERENCE: 38-21(51914)B
                                                                 Matches
                                                                              Query Match
Best Local Similarity
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SEQ ID NO 10
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CURRENT APPLICATION NUMBER: US/60/202,213
CURRENT FILING DATE: 2000-05-08
CURRENT FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 17986
                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PLANTS
                                                                                                                                                                                                                                                                                                                      APPLICANT: Andersen, Sco
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CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: US 60/202,213
PRIOR FILING DATE: 2000-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 09/654,617
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 09/684,016
PRIOR FILING DATE: 2000-10-10
                                                                                                                                                                              TYPE: DNA
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112 AGCTTCTATATTAAGCTTCGATGAGAAGA 140
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                                                         7.2%; but
100.0%; Pr
                                                                                                                                                                                                                                                                                                            NUCLEIC ACID MOLECULES
                                                                                                                                                                                                                                                                                                                                           Scott E.
                                                                                                                                              LIB3476-001-Q6-K2-A3
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Pred. No. 0.00015;
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Pred. No.
                                                                              Score 29;
Pred. No.
                                                                 Mismatches
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0.00015;
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0.00015;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 385;
                                                                                              Length 385;
                                                                 Indels
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; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3114-050-P1-K1-G7
US-09-565-306-82924
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US-09-850-147-40
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US-09-565-306-82924
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                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/565,306; CURRENT FILING DATE: US/09/565,306; CURRENT FILING DATE: 2000-05-04; CUMBER OF SEQ ID NOS: 83523 SEQ ID NO 82924 LENGTH: 393
TYPE: DNA
OPCANTO:
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           Sequence 40, Application US/09850147
GENERAL INFORMATION:
APPLICANT: Andersen, Scott E.
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: Nucleic Acid Molecules And
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51914)B
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APPLICANT: Hardeman, Kristine J.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51936)B
CURRENT APPLICATION NUMBER: US/09/865,439A
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 60/207,458
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NO 18142
LENGTH: 388
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Best Local S
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Matches 29; Conservative
                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Andersen, Scott E.
APPLICANT: Conner, Timothy W.
APPLICANT: Lalgudi, Raghunath V.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/09/850,147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: LIB3206-089-P1-N1-H4
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                                                                                                                                                                                                                                                                 112 AGCTTCTATATTAAGCTTCGATGAGAAGA 140
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nes 29; Conserv
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Conservative (
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Pred. No. 0.00015;
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0.00015
                                                     Other Molecules Associated With
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; SEQ ID NO 40

; LENGTH: 426

; TYPE: DNA

; ORGANISM: Sorghum bicolor

; OTHER INFORMATION: Clone ID: LIB3476-004-Q6-K1-A3

US-60-202-213-40
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US-09-850-147-1092
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Best Local S
SEQ ID NO 109:
LENGTH: 433
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                                                 APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Number: US/09/850,147
CURRENT APPLICATION NUMBER: US/09/850,147
CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: US 60/202,213
PRIOR FILING DATE: 2000-05-08
PRIOR FILING DATE: 2000-05-08
PRIOR APPLICATION NUMBER: US 09/654,617
PRIOR APPLICATION NUMBER: US 09/654,617
PRIOR APPLICATION NUMBER: US 09/654,016
PRIOR APPLICATION NUMBER: US 09/684,016
PRIOR FILING DATE: 2000-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 38-21(51914)A
CURRENT APPLICATION NUMBER: US/60/202,213
CURRENT FILING DATE: 2000-05-08
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PRIOR APPLICATION NUMBER: US 60/202,213
PRIOR FILING DATE: 2000-05-08
PRIOR APPLICATION NUMBER: US 09/654,617
PRIOR FILING DATE: 2000-09-05
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PRIOR FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 18014
                                       NUMBER OF SEQ ID NOS: 18014
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           135 AGCTTCTATATTAAGCTTCGATGAGAAGA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
hes 29; Conservative
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mes 29; Conservative
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Edgerton, Michael D
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Pred. No.
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0.00015;
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; NAME/KEY: unsure
; LCCATION: (1)..(433)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3476-004-Q6-K2-A3
US-09-850-147-1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Sorghum bicolor
; OTHER INFORMATION: Clone ID: LIB3476-004-Q6-K2-A3
US-60-202-213-1089
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US-60-207-458-54563/c
; Sequence 54563, Application US/60207458
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US-60-202-213-1089
; OTHER INFORMATION: US-60-207-458-54563
                                                             CURRENT APPLICATION NUMBER: US/60/207,458
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 152403
SEQ ID NO 54563
LENCTH: LECT
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SEQ ID NO 1089
LENGTH: 433
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Best Local Similarity
Matches 29; Conserv
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                                                                                                                                                     APPLICANT: Xu, Nanfei
TITLE OF INVENTION: PLANTS
TITLE OF INVENTION: PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NITTLE OF INVENTION: PLANTS
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                            ORGANISM: Zea mays
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                                                           LENGTH:
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nes 29; Conserv
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                                                                                                                                                                                                                      Sammons, R. Douglas
Shukla, Hridayabhiranjan
                                                                                                                                                                                                                                                                        Ruan, Yijun G
                                                                                                                                                                                                                                                                                   Hardeman, Kristine J.
La Rosa, Thomas J.
Lalgudi, Raghunath V.
                                                                                                                                                                                                                                                                                                                              Abad, Mark S. Conner, Timothy W. Deikman, Jill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                    Thomas
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             ID: uC-zmflb731234e12a1
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Pred. No.
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Pred. No.
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Query Match
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 AGCTTCTATATTAAGCTTTCGATGAGAAGA 140
Db 321 AGCTTCTATATTAAGCTTTCGATGAGAAGA 293

Search completed: January 2, 2003, 17:47:03

Job time: 3761 secs
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Minimum
Maximum
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Perfect score:
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length: 2000000000
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1: gb_ba:*
2: gb_htg:
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Pred. No.

is the number of results predicted by chance to have a

REFERENCE AUTHORS

Rattus.

1 (bases 1 to 173852)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1 ACO95235 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM		44	. 4. α ι ω ι	41 42	40	ມ ພ ອີດ	c 37	0 35 35		c 33	c 31		c 28	27	ر د د	24	23		c 19				c 14		c 11			c 7		ດ 4 ກ	-	2	Result No.	
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Harris, C., Harris, K., Harris, K., Harris, C., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, Howard, S., Huber, J., Hulk, S., Hume, J., Jackson, E., Homard, S., Huber, J., Hulk, S., Hume, J., Jackson, E., Jackson, R., Jolivet, S., Joudah, S., Karlson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E., Mahashwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Maheshwari, M., Nickerson, E., McLeod, M.P., Meador, M., Meir, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Mguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, M., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pimus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, T., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Stanley, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Williams, G., Williamson, A., Wieczyk, R., Wooden, S., Warley, K., Wu, Y., F., Zhou, J., Zorrilla, S., Nelson, D., Nerson, C., Warley, K., Weinstock, G. and Gibbs, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           worley.K.C.
Direct Submission
Submitted (16-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 173852)
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Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Worley, K.C.
Direct Submission
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On Jul 10, 20
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jul 10, 2002 this sequence version replaced gi:17942490
                                                                                                                                                   Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 92252 bases at least Q40
Consensus quality: 103231 bases at least Q30
Consensus quality: 111005 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: GDMA
Center clone name: CH230-10F21
----- Summary Statistics
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Bryant,N.P.,
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* consists of 79 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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1 (bases 1 to 176340)

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Nuzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrocks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Alsbrocks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Bunks,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cheveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
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***, 62 unordered
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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as soon as it is available and the be preserved.

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Hemsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Moi,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Worgan,M., Morris,S.,
Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., McLeod,M.P., Neery,J.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Pecry,J.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* CONSISTS OF 62 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baylor Plaza,
On Jul 19, 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 176340)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Worley, K.C.
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Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 127817 bases at least Q40
Consensus quality: 134179 bases at least Q30
Consensus quality: 139091 bases at least Q20
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Center clone name: CH230-54I13
Center clone name: Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: BCM
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DEFINITION Human 180 kDa bullous pemphigoid antigen 2/type XVII collagen (BPAG2/COL17A1) gene, exon 14.

SOURCE ORGANISM VERSION KEYWORDS SEGMENT ACCESSION Homo sapiens. 14 of 41 U76577.1

GI:1825501

JOURNAL MEDLINE PUBMED REFERENCE AUTHORS REFERENCE AUTHORS TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 369)
Gatalica, B., Pulkkinen, L., Li, K., Kuokkanen, K., Ryynanen, M., McGrath, J.A. and Uitto, J.
Cloning of the human type XVII collagen gene (COL17A1), and detection of novel mutations in generalized atrophic benign detection or ... epidermolysis bullosa epidermolysis bullosa 9012408 97164601 Eukaryota; Metazoa; Chordata;
Primates;

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352-365

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

Kuokkanen, K., Ryynanen, M.,

Submitted (29-OCT-1996) Dermatology, Thomas Jefferson University, 233 South 10th Street, Philadelphia, PA 19107, USA Location/Qualifiers 2 (bases 1 to 369)
Gatalica, B., Pulkkinen, L.,
McGrath, J.A. and Uitto, J.
Direct Submission Li, K., Ryynanen, M.,

Kuokkanen, K.,

FEATURES

JOURNAL TITLE

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MRRTQPTHMAVIFDTPEPTFRHELSPIYKGDRPSMPTELSEQIPYLHALIRALGIPLH
TLPGAEADDIIGTLAKRAEAMGHQVLISTGDKDMAQLVTEKVTLEDSFKEKPLDVDGV
                                                                                                                                                                TRQVALEQGFVETLLGRRLYTPDIDARNMMVRKAAERAAINAPLQGSAADIIKMAMIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEKFGVWPNQIIDYLTLMGDASDGIMGVPGVGAKTAAKLLTEYGSIGGILENVDKIKG
                                                                                                                                    VDKMLPKDQAKMLLQVHDELVFEVDEDIADELAPKLAEVMQSVLQISVPLVVEVGKGK
                                                                                                                                                                                    EEVTNDQRRQAKAVNFGLLYGMSEFGLIRQLGFTRQESQDYIKQYFHRYPGIYDYMQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rhodococcus
/strain="ATCC19558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="BPAG2/COL17A1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'db_xref="taxon:1833"
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Pred. No.
  Score
                                                                                 696
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Length 2964;
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TITLE
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669 CATAATGCCATCTGATGCAT 650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid c19612 is overlapped at the 3' end by cosmid c23A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein coding regions (CDS) have been predicted with the help of computer analysis using the Genefinder program in PomBase (an ACEDB database) with additional predictions for the branch-acceptor sites supplied by the program Sp3splice. CAUTION: It is possible that for any individual CDS we may have underestimated or overestimated the number of introns/exons or we may not have chosen the correct enlies decrease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 37000)
Oliver, K., Harris, D., Wood, V.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPAC19G12 37000
S.pombe chromosome I cosmid
Z97209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              splice donor/acceptor sites.

CDS are numbered using the following system eg SPAC5H10.01c. SP pombe), A (chromosome, 1), c5H10 (cosmid name), .01 (first CDS),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hinxton, Cambridge CB10 1SA E-mail: barrellesanger ac.us. On Feb 13, 1998 this sequence version replaced gi:2239193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (30-JUN-1997) Schizosaccharomyces pombe chromosome I sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe. Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrial energy transfer protein; pcyl; phosphatidylinositol-4-phosphate; pmsl; polysaccharide deacetylase; prenyl transferase; RNA-binding; RNP-1; splicing factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aldose reductase; carboxypeptidase Y; conserved hypothetical; cut20+; cyclosome/apc subunit cut20/apc4; dna mismatch repair protein; fatty acid hydroxylase; histone h2a-beta; hta2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Details of yeast sequencing at the Sanger Centre are available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       trehalose-phosphatase; tricarboxylate transport; tRNA-Leu;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/S_pombe/)
                                                                                                                complement(join(1.
                                                                                                                                                                                                                                   complement(join(1.
/note="SPAC19G12.01c, len:487"
                           'gene="cut20+"
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                                                                                                                                              /note="SPAC19G12.01c"
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                                                                                                                                                                                                           1451.
                                                                                                                                                                                                                                                                 /clone="cosmid c19G12"
                                                                                                                                                                                                                                                                                                                           /chromosome="I"
                                                                                                                                                                                                                                                                                                                                                                                 /strain="972h-"
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Schizosaccharomyces pombe"
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/gene="pms1"
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LYBATAQPAISTSYAEQASLAQVSKPLEPRLQKDSMRSSPLMEKVTASSERMKKKLA
LFASSTDTSMQKTIDSSEPLKQPINKESSKNULLLNDPSSPASTPVAKUTILNDIESUV
HNAESVSTLSSIPRTEQTSVANRIPSKTAALQKLKFFQSRPLDGLNKFSKKINISLSG
VQKDIVRSDALLKFSNKIGVVHDISDENQEDHLNLTVHKADFLAMRVVGQFNRGFIVV
VHGNULFIIDQHASDEKFNYEHLKSNLVINSQDIVLPKKLDLAATEETVLIDHIDLIR
RKGFGVAIDLNQRVGNRCTLLSVFTSKNVIFDTSDLLEIISVLSSHQIDIPFSSKLER
RKGFGVAIDLNQRVGNRCTLLSVFTSKNVIFDTSDLLEIISVLSSHQIDFFSSKLER
RLASKACRSSYNIGRALTISENNTIVRHLAELSKPWNCPHGRPTNRHLLRLKDI"
/note="SPAC19G12.03, len:320, LOW SIMILARITY:Yersinia pseudotuberculosis., CAB46604, hypothetical 33.7 kd protein., (293 aa), fasta scores: opt: 155, E():0.003,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="gtaagt, splice donor sequence"
complement(join(3623. .3702,3774. .4239,4342. .4758))
/gene="pms1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(2405..2417)
/gene="pms1"
/note="thacttctgtag, splice branch and
complement(2440..2445)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LCAVGQVIISTATQNEAPKGVQLNLDHEGSLKDKLTIPFQRGTSVMVNDLFCTLPVRR
KLLEKNYKREFSKAISLLQAYATISTNRFMVYHGTKNSGKLLOLSTNSKKDMKLNIM
KLEKNYKREFSKAISLLQAYATISTNRFMYVHGTKNSGKLLOLSTNSKKDMKLNIM
NVFGTKVSSLLIPMNDGIIGQYISRFHYGSTRAKSNERQMLFINRTUKLAVIVG
VFKPYSMAQSPFFAINLRITNGTIDINVSPDKKSVFLSEEDSIIEFIKNSLQNLCESC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4342
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HSITNDLAYHYLICKGGTNISLKTLYMPLLKNDLGSIVDIATMSTRMQHLVRYLEEVL
NAMYEEFDNYFKSEASFIKTFOALVSKYSDTFFSLOLELYQFIMNGIPSDLLKEWIN
ERVGDRYLKNWERAMVNSYTSLIIFCQEFVIPACERLFYLLSSARGKSIWGHMKGNTL
LDAKLVEDCLARLGYLONNYFSFLNCLFEEKKYMKHFISWLNYAIVEFNTSEPSSIPP
QEIIEHINETVIYIRHSLFRSKLTSYFMCTKPLQLRD
COMPLEMENLJOIN(2169. .2404,2446. .3702,3774. .4239,
                                                                                                                                                                                                                                                                               /note="gtaagt, splice donor
complement(4468. .4488)
                                                                                                                                                                                                                                                                                                                                                                      /note="ctaactgaatgtag, splice branch and acceptor"
complement(4336. .4341)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="gtatgt, splice donor sequence"
complement(4240. .4253)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repair protein Score 529.60" complement(3703. .3719)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SWISS-PROT: P54280"
/translation="MSTVKPIDANTVHKICSGQVITDVASAVKELVENSLDSGATTIE
IRFKNYGINSIEVVDNGSGIDAGDYESIGKKHFTSKITDFEDLEALQTFGFRGEALSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="pms1"
/note="SPAC19G12.02c"
complement(join(2169.
4342. .4767))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4342
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LTCSNHLICCRSNSQRIWDVDFHDLEATELCWNHDGNLIVVGFKNGELKIIDSSTGHL
VEQRPASRDLAVLMITWAMQETIVNEKRNDFLFDATAYMPLLGTLPSSAKEERIFSSK
                                                                                                                                                                                                                                                                                                           /gene="pms1"
/note="gtaagt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="DNA mismatch repair protein
/protein_id="CAB10113.1"
/db_xref="GI:2239195"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /4342. .4/0/)
/gene="pms1"
/note="SPAC19G12.02c, len:794"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="cyclosome/apc subunit cut20/apc4"
/protein_id="CAB53521.1"
/db_xref="GI:5791550"
                                                                                                                                                        /gene-"SPAC19G12.03"
                                                                                                                                                                                                                                                /gene="pms1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="pmsl"
                                                                                                /gene-"SPAC19G12.03"
                                                                                                                                                                                                                    note="PS00058 DNA mismatch"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="pms1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="Match to PF01119 DNA_mis_repair,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene-"pmsl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label=cut20+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2404,2446.
                                                                                                                                                                                                                    repair proteins mutL"
                                                                                                                                                                                                                                                                                                           sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .3702,3774. .4239,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pms1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and acceptor'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acceptor"
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Best Local
15917
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                                              339 TTTCTGGTTTCTTTTGAACA 358
TTTCTGGTTTCTTTTGAACA 15936
                                                                                                                     Similarity
                                                                                             5.0%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="SPTREMBL:013843"
/translation="MeakKiyaqaltdeafapfgsvvqqkddvkmysanggtakkylk
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AAFNYENGVAEDDCQVQSTESPIEVFIKIST"
8397. 9272
                                                                                                                                                                                                                                                                                                                                                /gene="SPAC19G12.05"
/note="Pfam match to entry mito_carr PF00153,
Mitochondrial carrier proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SPAC19G12.05"
8397..9272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SPAC19G12.04"
/note="SPAC19G12.04, len:191, SIMILARITY:Saccharomyces
/note="SPAC19G12.04, len:191, SIMILARITY:Saccharomyces
cerevisiae, DAL3_YEAS7, ureidoglycolate hydrolase, (195
aa), fasta scores: opt: 360, E():5e-17, (36.5% identity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="SPAC19G12.04"
6888. .7463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MYETRDLIGNAGKPVDINPWPNNSKIAVSPVVNYEEGGERSLLY
EDEGFETFLIEAGLMPFPNRPVRERSIESCFEYGSRCGFWRILMIKKKHKVPFTCWAI
GQAVEKNPVVGAMEEAGCEVGSHSHRWINYEGVPFTEYEHIKKSVQAIQKASPSNK
APRSWYTGRASLNTRKLVCQVYKDLGLPQPFDSDEYNDDYPYWYADPLASKPGAEDNK
GLLIVPYTLEVNDMKYAVAPGFCNSDDFYTYARDAFDVLYEEGLEGAPKMMTIGLHCR
                                                                                                                                                                                                                                                                                                                                                                                                                              8397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                YCTQPIDTVKSRMQSLSASKEYKNSIHCAYKILTQDGLLRFWSGATPRLARLILSGGI
VFTVYEKVMEILKPF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPRTVLAGLGAGVAESVLVLTPFESIKTAIIDDRKRPNPRLKGFLQASRIIVHENGIR
GLYRGLAATVARQAANSGVRFTAYNSIKQSLQSRLPPDEKLSTVTTFLVGSVAGIITV
                                                                                                                                                                                                                        complement(10121. .10516)
                                                                                                                                                                                                                                             signa ture"
                                                                                                                                                                                                                                                                                                                             8505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative tricarboxylate transport protein"
/protein_id="CAB10116.1"
/db_xref="GI:2239198"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="SPAC19G12.05, len:291, SIMILARITY:Saccharomyces
cerevisiae, TXTP_YEAST, tricarboxylate transport protein,
(299 aa), fasta scores: opt: 738, E():0, (49.0% identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5608.
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/protein_id="CAB10114.1"
/db_xref="GI:2239196"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {	t LQLYRNVEGTKAKLPPFGLEWYRGCSTVIVGNSLKAAVRFFAFDSIKKSLSDEHGHLT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in 290 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SPAC19G12.05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTGRPGRFRGLQKLMEHITSKEGVWVATREQIAQAWSAKHPYKA"
                                                                                                                                                                                                /gene="hta2"
                                                                                                                                                                                                                                                                         note="PS00215 Mitochondrial energy transfer proteins"
                                                                                                                                                                                                                                                                                                 /gene="SPAC19G12.05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="SPTREMBL:013844"
/translation="MSTVAKTNPKSSNKPGPVKSIIAGGVAGAIEISTTYPAEFAKTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label=SPAC19G12.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative ureidoglycolate hydrolase"
/protein_id="CAB10115.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label=SPAC19G12.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SPAC19G12.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="SPTREMBL:013842"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=SPAC19G12.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (27.5% identity in 
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Pfam match to entry PF01522 Polysac_deacet"
                                                                                             0;
                                                                                                                       Score 20;
Pred. No.
                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265
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                                                                                                                                               DB 8;
                                                                                                                     4.6;
                                                                                                                                            Length 37000;
                                                                                                  Indels
                                                                                                0;
                                                                                                Gaps
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REFERENCE
AUTHORS
TITLE
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
AC100210/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cook, P., PitzHugh, W., Gaye, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Junes, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Norman, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Reil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Ries, C., Rogov, P., Raman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Viell, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zahnoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birren, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC100210
Mus musculus clone RP23-59M9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus, clone RP23-59M9
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                                                                                                                                                                                                                                                                                                              contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This record contains 74 individual sequencing reads that have not been assembled into
                                                                                                                                                                                                                                                         be
                                                                                                                                                                                                                                                                                        the record
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 59237)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeats were identified using RepeatMasker:
t, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L14347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: L143 Center clone name: 59_M_9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: WIBR
                                                                                                                                                                                                                                                         preserved.
                                                                                                        1593
1 693: contig of 693 bp in length
194 793: gap of 100 bp
194 1492: contig of 699 bp in length
193 1592: gap of 100 bp
193 2294: contig of 702 bp in length
195 2394: gap of 100 bp
195 3040: contig of 646 bp in length
196 100 bp
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                                                                                                                                                                                                                                                                                  is updated, the accession number will
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, LOW-PASS SEQUENCE SAMPLING.
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13447 13546: contig of 708 bp in length

13447 13546: gap of 100 bp

13547 14237: contig of 691 bp in length

14238 14337: gap of 100 bp

14338 15022: contig of 695 bp in length

15023 15122: gap of 100 bp

15123 15122: gap of 100 bp

15814 15913: gap of 691 bp in length

16618 16717: gap of 100 bp

16618 16717: gap of 100 bp

17395 17404
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20567 20666: gap of 100 bp
20667 21375: contig of 709 bp
21376 21475: gap of 100 bp
21376 22481: gap of 100 bp
22182 22281: gap of 100 bp
22282 22984: contig of 703 bp
22282 22984: contig of 703 bp
22385 23084: gap of 100 bp
23756 23855: gap of 100 bp
23756 23855: gap of 100 bp
23856 24562: contig of 671 bp
23856 24562: contig of 707 bp
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17394: contig of 677 bp in len

17395 17494: gap of 100 bp

17495 18188: contig of 694 bp in lend

18189 18288: gap of 100 bm

18289 18966: contig
                                                                                                                        27800 27899: gap of 100 bp
27900 28616: contig of 717 bp
28617 28716: gap of 100 bp
28717 29419: contig of 703 bp
29420 29519: gap of 100 bp
29520 30212: contig of 693 bp
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27096 27799: c
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25486 2619
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19067 19749: contig of
19750 19849: gap of
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93 26292: gap of 100 bp

93 26995: contig of 703 bp ir

16 27095: gap of 100 bc

6 27706
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2 7107: contin - 1
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25385; cont
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31935: gap of
32635: contig
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8704: con
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31835: contig of 735
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55259: contig
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45615: contig of 708 bp in
715: gap of 100 bm
46420: con+1-
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100 bp in length
42: 52: contig of 706 bp in length
52: gap of 100 bp
50447: contig of 695 bp in length
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48044: contig of 717 bp in
44: gap of 100 bp
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44000: contig of 697 bp in
00: gap of 100 bp
44807: contig of 707 bp in
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g of 696 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted (25-APR-2002) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zainoun, J., Zembel Direct Submission
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Mus musculus, clone RP24-527P22
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Birren, B., Linton, L.,
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       overlap relationships among clones to be deduced However, it should not be assumed that this clone will be sequenced to completion. In the event the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This record contains 75 individual sequencing reads that have not been assembled into
                                                                                                                                                                                                                                                                                                                                                                                                                                                    be preserved.
                                                                                                                                                                                                                                                                    717: contig of 717 bp in length
718 817: gap of 100 bp
818 1532: contig of 715 bp in length
1533 1632: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: WIBR Web site: http://www-seq.wi.mit.edu
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        5689: gap
6395:
                                                                 4882: gap
5589:
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3961: contig of 706 bp
4061: gap of 100 bp
4782: contig of 721 bp
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> Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pherre, N.,
> Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
> Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
> Landers, T., Lehoczky, J., Levine, R., Lindblad Toh, K., Liu, G.,
> McCarthy, M., McEwan, P., McKernan, K., McIdrim, J., Meneus, L.,
> McCarthy, M., McEwan, P., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
> Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
> Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D.,
> Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
> Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
> Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
> Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
> Topham, K., Travers, M., Travis, N., Trajilio, J., Vassiliev, H.,
> Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
> Zahnoun, J., Zembek, L., Zimmer, A. and Zody, M. A (bases 1 Coving)
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6495: gap 7213:

...: contig c ...: gap of 8030: cr 0: gap of 8860: con

100 - 717 ď

bp in bp in

length

12979 13078: gap of 100 bp 110797 13772: contig of 694 bp in 16 13773 13872: gap of 100 bp 13873 14587: contig of 715 bp in 16 14588 14687: gap of 100 bp 14688 15433: contig of 746 bp in 16 15434 15533: gap of 100 bp 15534 16338: contig of 765 bp in 16 16530 16338: contig of 705 bp in 16

bp in length

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contig of

100 bp of 730 bp in ) 100 bp of 719 bp

9779:

9: gap of 100 10515: contig of 73

1350 11449:

0615: gap of 100 bp 11349: contig of 734 k 1449: gap of 100 bp 12165: contig of 716 bp 2265: gap of 100 bp 12978: contig of 713 b

length

length

12265:

p of 100 bp contig of 713 bp

bp in bp in bp in bp in in

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length

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KEYWORDS
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Best Local S
Matches 20
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                                                                                                                           TTGACTTCAGGTGGACAATT 4296
                                                                                                                                            TTGACTTCAGGTGGACAATT 244
      Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
1 (bases 1 to 84767)
                                                 AC004149.1
HTG.
                                                                 Homo sapiens chromosome AC004149
                                                                                                                                                            . Similarity
20; Conserv
                                                                                  AC004149
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3 38796: contig of 70
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7 39620: contig of
1 39720: gap of
1 40428: contig of
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3 37195: contig c
6 37295: gap of
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43740: con
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41251: ~~
751.
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42908: contig of 737
McKernan, K.,
                                                                                  84767 bp
                                                                         17, clone hCIT.501_0_10, complete sequence.
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g of 708 bp
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               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Richardson, P. and
                                                                                  PRI 06-JUN-2000
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21739 21838:

length

21194:

24272: 23450: 22633:

21838: gap of 100 bp 122533: contig of 695 bp in 1e 22633: gap of 100 bp 100 bp 23450: gap of 100 bp 
26696:

25885: 25069:

bp in length

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length

20278 20377:

19550:

16338: gap of 100 bp 11 length 17165: gap of 100 bp in length 17165: gap of 100 bp in length 17871: contig of 706 bp in length 17971: gap of 100 bp in length 18755: gap of 100 bp in length 18755: gap of 100 bp in length 19550: contig of 684 bp in length 19550: gap of 100 bp 20277: contig of 727 bp in length 20377: gap of 100 bp 21784: contig of 717 bp in length 21194: gap of 100 bp 21198: contig of 717 bp in length 21198: contig of 544 bp in length 21138: contig of 544 bp in length 21138: contig of 544 bp in length

17872 17971: 18656 18755:

27519: gap of 100 bp 27520 28347; contig of 728 bp in length 28248 28347; contig of 728 bp in length 28048 29064; contig of 717 bp in length 29065 29164; gap of 100 bp 29165 29875; contig of 711 bp in length 29876 29975; gap of 100 bp 100 bp 29876 29975; gap of 100 bp 
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30686: contig of 711 bp 30786: gap of 100 bp 31500: contig of 714 bp 1 31500: gap of 100 bp 32302: contig of 702 bp 1 32402: gap of 100 bp 32307: contig of 702 bp 103207

length

30786:

FEATURES SOURCE	TITLE JOURNAL	TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS
	Cerny, J. Cooke, P., Daly, M.J., Depayre, E., Devon, K., Dewar, K., Donelan, L., Durette, B., Etemadi, S., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Gensheimer, S., Geraigery, K., Gilmartin, T., Grant, G., Gray, D., Hagos, B., Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Kann, L., Linton, L., Macdonald, P., Marguis, N., McDewan, P., McGurk, A., Meldrim, J., Molla, M., Morris, W., Morrow, J., Nachman, A., Nahf, R., Naylor, J., O'Connor, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rollins, G., Rossello, R., Roy, A., Shyam, R., Stange-Thomann, N., Stilwell, J., Stone, C., Strickland, C., Subramanian, A., Sydney, K., Tang, L., Vassiliev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W. J., Zhao, J. and Zody, M. Direct Submission AL Submitted (06-JUN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 23, 1998 this sequence version replaced gi:2980974. All repeats were identified using RepeatMasker: Smit, A.F.A. &	Piecet Submission Direct Submission Direct Submission Direct Submission Example (16-FEB-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 84767) Birren,B., Fasman,K., McKernan,K., Nusbaum,C., Richardson,P., Lander,E., Allen,N., Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Boatin,C., Boutwell,C., Byrne,S., Cantu,C., Castle,A., Cerny,J., Cooke,P., Daly,M.J., Depayre,E., Devon,K., Dewar,K., Benn,J., DuRette,B., Etemadi,S., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Gardyna,S., Gensheimer,S., Geraigery,K., Gilmartin,T., Grant,G., Gray,D., Hagos,B., Harris,K., Donelan,L., Dwhand,J.C., Hui,L., Jacotot,L., Kann,L., Linton,L., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., Meldrim,J., Molla,M., Morris,W., Morrow,J., Nachman,A., Nahf,R., Naylor,J., O'Connor,T., Pavlin,B., Peterson,K., Riley,R., Roberts,D., Rollins,G., Rossello,R., Roy,A., Shyam,R., Stange-Thomann,N., Stilwell,J., Stone,C., Strickland,C., Subramanian,A., Sydney,K., Tang,L., Vassiliev,H., Vo,A., Wagner,A., Wang,B., Wheeler,J., Wu,Y., Ye,W.J., Zhao,J. and Zody,M. Direct Submitsed (23-MAR-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 84767) S Birren,B., Fasman,K., McKernan,K., Nusbaum,C., Richardson,P., Lander,E., Allen,N., Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Boatin,C., Boutwell,C., Byrne,S., Cantu,C., Castle,A.,	Lander, E.  Homo sapiens chromosome 17, clone hCIT.501_0_10  Unpublished  £ 2 (bases 1 to 84767)  £ Birren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P.,  Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R.,  Boutwell, C., Byrne, S., Cantu, C., Castle, A., Cerny, J., Cooke, P.,  Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Deckerly, R.,  Boutwell, C., Byrne, S., Cantu, C., Castle, A., Cerny, J., Davette, B.,  Etemadi, S., Ferreira, P., Forrest, C., Funke, R., Gage, D., Gardyna, S.,  Etemadi, S., Geraigery, K., Gilmartin, T., Gray, D., Hagos, B.,  Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Linton, L.,  MacKenzie, J., Marquis, N., McEwan, P., McGurk, A., Meldrim, J.,  Molla, M., Morris, W., Morrow, J., Nachman, A., Naylor, J., O'Connor, T.,  Pavilin, B., Peterson, K., Rauganath, S., Riley, R., Roberts, D.,  Rollins, G., Rossello, R., Roy, A., Shyam, R., Soohoo, S.,  Stange-Thomann, N., Stilwell, J., Stone, C., Strickland, C., Sydney, K.,  Tang, L., Vassillev, H., Vo, A., Wanner, A., Wheeler, T., W., Y.
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 Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M.,
                          Birren,B.,
                                                                                                                                              Homo sapiens
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HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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Horton, L., Hulme, W., Illev, I., Johnson, R., Johnson, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Grand-Pierre, N., Hagos, B., Gardyna, S., Grand-Pierre, N., Hagos, B., Gardyna, S., Gardyna, S., Grand-Pierre, N., Hagos, B., Gardyna, S.,                                                                                                                     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Ye, W.J., Young, G., Vashing, R., Vo, A., Wilson, B., Wu, X., Nahama, D., Ye, W.J., Young, G., Vashing, R., Vo, A., Wilson, B., Wu, X., Nahama, D., Ye, W.J., Young, G., Vashing, R., Vo, A., Wilson, B., Wu, X., Nahama, D., Ye, W.J., Young, G., Vashing, R., Vo, A., Wilson, B., Wu, X., Nahama, D., Ye, W.J., Young, G., Vashing, R., Vo, A., Wilson, B., Wu, X., Nahama, R., W., X., W., Y., W
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                                                                                                                                                                                                                     Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L.,
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Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
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Contact: sequence_submissions@genome.wi.mit.edu
1 68585: contig of 68585 bp in length 68586 68685: gap of 100 bp 68686 80011: contig of 11326 bp in length 80012 80111: gap of 100 bp 80112 108353: contig of 28242 bp in length 108354 108453: gap of 100 bp 108454 1184459: contig of 20006 bp in length
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (18-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enguiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 20, 2000 this sequence version replaced gi:8452481.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                         The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw:, SWISSPROT; TT:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL138761 141970 bp DNA linear PRI 28-JUL-2000 Human DNA sequence from clone RP11-16H23 on chromosome 10. Contains the gene KIAA0204 (HSLK) for a protein kinase, the COL17A1 gene for collagen type XVII alpha i (BP180), ESTs and GSSs, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/HGP/Chr10
RP11-16H23 is from the library RPCI-11.1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                            Mapping Group.
http://www.sand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          feature key.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone="RP11-16H23"
/clone_lib="RPCI-11.1"
6. .478
                                                                          /db_xref="taxon:9606"
/chromosome="10"
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/clone="RP11-414J4"
/clone_lib="RPCI-11 Human
/33887 c 34863 g 30464
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/db_xref="taxon:9606"
/chromosome="15"
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COL17A1; collagen; HSLK;
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/note="MIR repeat: matches 173...
7764. 7857
/note="12 repeat: matches 2456...
7858. 8152
/note="AluSx repeat: matches 1...
8153. 8349
/note="12 repeat: matches 2548...
8412. 8728
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/note="AluSx repeat: m
3051. .3567
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13914. .13979
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12900. .13206
                                                                                                                                                join(<14114. .14278,16037. .16085,16423. .16572,22338. ...
22558. .22752,23306. .23387,24883. .25011,25611. .26566,
29000. .29130,29351. .29474,31616. .3179,34255. .34347,
41599. .41728,42223. .42347,43173. .43361,43927. .44052,
45059. .45172,49013. .52672)
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join(<14114..14278,16037..16085,16423..16572,22338..
22558..22752,23306..23387,24883..25011,25611..26966,
29000..29130,29351..29474,31616..31795,41599..41728,
42223..42347,43173..43361,43927..44052,45059..45172,
                                                                                                                                                                                                                                                                                                                     /note="AluY 13207. .1391
                                                                                                                                                                                                                                                                                                                                                                                   /note="L2 repeat: matches 2611. .2697 of consensus" 12514. .12899
                                                                                                                                                                                                                                                                                                                                                                                                                   12296. .12415
/note="MIR repeat:
12398. .12485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="AluSg
11314. .11808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MER82 repeat: matches 2. 7560..7611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L1ME repeat: 3725. .5542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: GSS: 41. .330
                                                                                                                                                                                                                                    14114. .52672
/gene="bA16H23.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11956.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MER34 repeat:
11819. .11942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10108.
                                                 /evidence=not_experimental
join(<14114...14278,16037.
                                                                                    note="match: cDNAs: Em:D88425 Em:AB015718"
                                                                                                     (isoform 2))"
                                                                                                                                  /gene="bA16H23.1"
                                                                                                                                                                                                                                                                   note="L1M4 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MER85 repeat: matches 1.
12000. .12162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8412. .8728
/note="MER44A repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6285. .6488
/note="MIR repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MER82 repeat: matches 446. .653 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="L1ME1
                                                                                                                    /product="bA16H23.1.2 (protein kinase KIAA0204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="MIR repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="MER20 repeat: matches 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .11985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .10414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .11808
                                                                                                                                                                                                                                                                                                                                 repeat: matches 1. .307
                                                                                                                                                                                                                                                                                                    repeat: matches 5561. .6305 of consensus
                                                                                                                                                                                                                                                                                                                                                                   repeat: matches 5186. .5561 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     matches 18.
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                                                                                                                                                                                                                                                                      matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     matches 1.
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                                                                                                                                                                                                                                                                     5186. .5253 of consensus"
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Em: AW402772 Em: AAA798865 Em: AL120836 Em: C18798 Em: AAA602772 Em: AAA798865 Em: AL120836 Em: C18798 Em: AAA880588 Em: AA1088714 Em: AAA798865 Em: AA268478 Em: H31623 Em: AAA880588 Em: AA108474 Em: AAA91329 Em: D82765 Em: AA356218 Em: AAA86058 Em: AA06427 Em: AA491329 Em: AAA763026 Em: AA756218 Em: AA436405 Em: AA1559709 Em: D53990 Em: AAA403026 Em: AA702324 Em: AA123337 Em: C15395 Em: AA362324 Em: AA03026 Em: AA172334 Em: AA132337 Em: C15395 Em: AA17494 Em: AA398426 Em: AA772565 Em: AA1338645 Em: AA1378364 Em: AA124068 Em: R88093 Em: C14927 Em: AA323083 Em: AA1378364 Em: AA1640071 Em: AB8093 Em: AA4517 Em: AA323083 Em: AA137836740 Em: AA4604225 Em: AA724517 Em: R78600 Em: AA463393 Em: AA002195 Em: AA100071 Em: AA367441 Em: AA307061 Em: AA463393 Em: AA021059 Em: AA264446 Em: AA307061 Em: AA4648 Em: N58456 Em: AA644445 Em: H134377 Em: C15275 Em: A1337832 Em: AA042144 Em: AA365137 Em: C15275 Em: A1337832 Em: AA922145 Em: A1367042 Em: AA4648 Em: N9850 Em: AA367240 Em: AA367240 Em: AA367218 Em: AA644445 Em: AA645471 Em: AA367240 Em: AA367240 Em: AA367218 Em: AA36444 Em: N78546 Em: AA367240 Em: AA367218 Em: AA367333 Em: AA367240 Em: AA367333 Em: AA36735 Em: A13684 Em: AA36735 Em: A13685 Em: AA36735 Em: A13685 Em: AA36735 Em: A13685 Em: AA3675 Em: A13685 Em: AA3675 Em: A13685 Em: AA3675 Em: A13685 Em
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22558. ...22752,23306. ...23387,24883. ...2311,25611. ...26966,
29000. ...2130,29351. ...29474,31616. ...31795,41599. ...41728,
42223. ...42347,43173. ...43361,43927. ...44052,45059. ...45172,
                                                                                                                                                                                                        LKQQLKDQYFMQRHQLLKRHEKETEQMQRYNQRLIEELKNRQTQERARLPKIQRSEAK
TRMAMFKKSLRINSTATPDQDRDKIKQFAAQEEKRQKNERMAQHQKHENQMRDLQLQC
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                                                                                                              LOEQEVFFKMTGESECLNPSTQSRISKFYPIPSLHSTGS"

Join (<14114 . .14278, 16037 . .16085, 16423 .
                                                                                                                                                                                EANVRELHQLQNEKCHLLVEHETQKLKELDEEHSQELKEWREKLRPRKKTLEEEFARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAC00587.1"
/db_xref="GI:9588136"
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AUTHORS
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     JOURNAL
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Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 11, clone RP11-34A20 Unpublished
                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 145695)
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Db 83751 GACATGTGCCAGGAGAAGGG 83770
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                                                                                                                                                                                                                         Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Enjiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
HOmo sapiens genomic DNA
Published Only in DataBase (2000)
2 (bases 1 to 143620)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (24-APR-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                             (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
On Mar 16, 2001 this sequence version replaced gi:12381916.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
                                                                                                                 Location/Qualifiers
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Db 122317 GTGTTAATTGTGGAGGTTCA 122298 292 GTGTTAATTGTGGAGGTTCA 311 AC015690 AC015690.3 GI:9107982 HTG; HTGS\_PHASE0. Homo sapiens chromosome SEQUENCE SAMPLING. 20; Conserv Conservative 100.0%; 5.0%; Score 20; DB 9 100.0%; Pred. No. 4.5; ive 0; Mismatches 145695 bp DNA linear ne 11 clone RP11-34A20 map 11, DB 9; Length 143620; 0; Indels HTG 13-JUL-2000 LOW-PASS 0; Gaps

/clone="RP11-140023" 28357 c 29648 g 43900 t

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/map="11q"

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COMMENT
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Direct Submission

Direct Submission

Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Submitted (17-NOV-1991)

On Jul 13, 2000 this sequence version replaced gi:6910854.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

Smit, A.F.A. & Green, P. (1996-1997)
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------ Project Information
Center project name: L1347
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Mammalia; Eutheria;
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100 bp
01658: contig of 797 bp:
19 61758: gap of 100 br
62531: contig
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100 bp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62531: contig of 773
531: gap of 100 1
63427: contig of 796
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1761: contig of 793 bp
gap of
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Primates;
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of 779 bp in
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of 773 bp in
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SEQUENCING
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Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kalls, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Wy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Dlaz, J.S., Dodge
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S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Carthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McCarthy, M., McPheeters, R., McCarthy, M., McCa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: Project Information
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55167 70769: contig of 15603 bp in length
70770 7089; gap of 100 bp
70870 145870: contig of 75001 bp in length
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
                                                                                                                                                                                                                                               1. .145870
                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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KEYWORDS
SOURCE
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                                                                                                         Homo sapiens of SEQUENCE, 19 of AC036150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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2 (bases 1 to 151937)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujlyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens genomic DNA, chromosome 11q, clone:RP11-264L21,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                    Homo sapiens
                                                                   HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                            AC036150
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AP001980.5
                                                                                       AC036150.2 GI:7705190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-MAY-2000) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone="RP11-39201"
/clone_lib="RPCI-11 Human Male
/clone_lib="35452 g 36198 t
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/db_xref="taxon:9606"
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28003 c 27962 g 46603 t
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Direct Submission

AL Submitted (07-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

CE 3 (bases 1 to 156186)

CE 3 (bases 1 to 156186)

CE 3 (bases 1 to 156186)

RS Bairren.B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boyuslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., LaRocque,K., Lamazares,R., Landers,T., Leboczky,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Voya,T., Morton,V., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Stange-Thomann,N., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stolanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Young,G., Zainov,A., and Zodv,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Research, 320 Charles Street, Cambridge, MA 02141, USA on May 4, 2000 this sequence version replaced gi:7523818. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Homo sapiens chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731 Consensus quality: 147950 bases at least Q40 Consensus quality: 153513 bases at least Q20 Consensus quality: 153513 bases at least Q20
                                                                                                                                                                                                                                                  Center project name: L9050
Center clone name: 264_F_13
-----Summary Statistics
Sequencing vector: M13; M77815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Project Information
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98527 11.

115881 115980: 9ax

115981 134149: contig ...

* 134150 134249: gap of 10.

* 134250 156186: contig of 21

Location/Qualifiers 156186

156186 ...
""Homo sapier ...4606"
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24400 24499: gap of 100 bp

24500 30398: contig of 5899 bp in length

30399 30498: gap of 100 bp

30499 37678: contig of 7180 bp in length

30499 37678: contig of 7180 bp in length

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45561 45560: gap of 100 bp

45561 45660: gap of 100 bp

53285 53284: gap of 100 bp

53285 63459: contig of 7524 bp in length

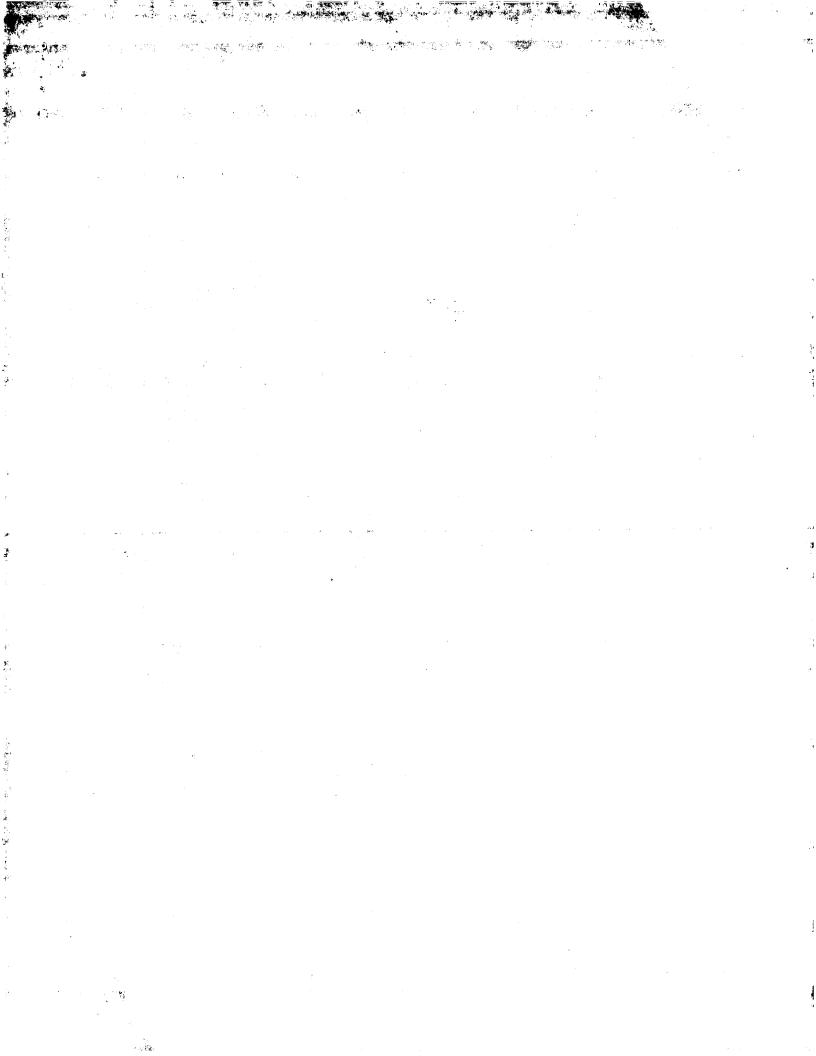
53460 63560
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548 647: gap of 100 bp
648 3155: contig of 2508 bp in length
3156 3255: gap of 100 bp
3256 6384: contig of 3129 bp in length
6385 6484: gap of 100 bp
6485 9217: contig of 2733 bp in length
9218 9317: gap of 100 bp
13051 13150: gap of 100 bp
13151 16192: contig of 3733 bp in length
13051 13150: gap of 100 bp
13151 16192: contig of 3734 bp in length
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Insert size: 154386; sum-of-contigs
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16293 20043: contig of 3751 bp in length
20044 20143: gap of 100 bp
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contig of 17254 bp in
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Search completed: January Job time: 3743 secs

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                                                                                  Length 156186;
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Database :
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Perfect score:
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                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Result No.		Query Match Length DB	Length	BB	ID	Description
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ω	19	4.7	1444	21	AAC46559	Zea mays DNA
c 4	19	4.7	2016	23	AAS69866	DNA encodi
տ	19	4.7	2020	23	AAS82153	DNA encoding novel
σ	18	4.5	360	20	AAV89959	EST clone CS765.
7	18	4.5	872	21	AAC99130	Human pancreatic
8	18	4.5	899	22	ААН06889	Human cDNA
9	18	4.5	1149	21	AAA51824	Human melanocortin

Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger Reinhard C, Randazzo F, Kennedy GC, Pott D, Kassam A, Lamson G Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I; Leshkowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B;

(CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.

WPI; 2001-530177/58

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44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
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4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.5		4.5	4.5	4.5	4.5										4.5	5
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AAC99118 ABV50321	ABN90603	ABA13256	AAH53375	AAH52447	AAH08928	AAV87181	ABN20928	AAH87393	аан86650	AAC29123	AAX40512	AAQ60849	AAC10644	AAC16115	AAQ60752	ABL66186	ABN96499	AAS09301	AAH51601	ABA15643	AAS28713	AAS30020	AAS28714	AAS30021	AAS84715	AAS73822	AAS69913	ABK09751	AAH14592	AAS72090	AAS84712	AAS73815	AAC69571	AAH14264
Human pancreatic c Human prostate exp	Staphylococcus epi	Human nervous syst	epidermidis	s. epidermidis ope	Human cDNA clone (	EST clone BD489.					Human secreted pro			Human secreted pro	Human brain Expres			Human schizophreni	Human chromosome 1	Human nervous syst	Genomic sequence #	Human lung antigen	Genomic sequence #	Human lung antigen	encoding	DNA encoding novel	DNA encoding novel	Human ovarian tumo	an cDNA s	encoding	DNA encoding novel	DNA encoding novel		Human cDNA sequenc

## ALIGNMENTS

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RESULT 1
AAS38626
09-MAR-2000; 2000US-0188609.
                                                                                        09-MAR-2001; 2001WO-US07787.
                                                                                                                                  Homo sapiens.
                                                                                                                                               Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic; ss
                                                                                                                                                             Novel human diagnostic and therapeutic gene #1684.
                                                                                                                                                                           17-DEC-2001 (first entry)
                                                                                                                                                                                           AAS38626;
                                                                                                                                                                                                       AAS38626 standard; cDNA; 324
                                                                                                       13-SEP-2001.
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RESULT 2
ABN64583
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specification,
                                    gene
                                              The invention relates to an isolated polynucleotide (ABN27253-ABN33262) with cytostatic activity. The polynucleotide is used to produce a polypeptide, to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and to inhibit tumour growth. The polynucleotide is used as a probe in mapping and tissue profiling. The encoded polypeptide and antibodies to the polypeptide can also be used for therapeutic and diagnostic purposes. The polynucleotide is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous. They can also be used to inhibit tumour growth by modulating expression of a gene product. AAS36943-AAS39338 represent novel human diagnostic and therapeutic coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to new polynucleotides and polypeptides, useful for diagnosis and treatment of breast, lung and colon cancer. The sequences can be used in detecting differentially expressed genes correlated with a
                                                                                                                                                                             New nucleic acid for producing a expressed genes correlated with and inhibiting tumor growth -
                                                                                                                                                                                                                                      WPI; 2002-241905/29.
                                                                                                                                                                                                                                                              Escobedo J,
Lamson G, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human;
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                                                                                                                                                                                                                                                                                                     (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
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                                    therapy.
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                        The sequence data
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                                                                                                                                                      SEQ ID NO 4550; 883pp + Sequence Listing; English.
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Scott EM,
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          but
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"Zhang"
          was obtained
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er; tumour; gene;
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                        for this patent did
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ang G, Kassam Å,
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          atent did not form part of the printe electronic format directly from WIPO
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ot D, Labat
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Matches 19
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119-APR-1999
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23-APR-1999
23-APR-1999
30-APR-1999
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06-MAY-1999
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11-MAY-1999
11-MAY-1999
                             18-MAY-1999;
19-MAY-1999;
20-MAY-1999;
21-MAY-1999;
24-MAY-1999;
25-MAY-1999;
27-MAY-1999;
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29-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
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14 - MAY - 1
       01-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                             promoter; termination
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                                                                                                                                                                                                                                                                                                               2000EP-0301439
      990S-0130510
990S-0131449
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990S-013428
990S-0134218
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990S-0127462.
990S-0128234.
990S-0128714.
990S-0129845.
990S-0130077.
990S-0130449.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                              sequence; corn;
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07-JUN 1999
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Query Match 4.7%;
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Matches 19; Conservative
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S-0149175.
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S-0151066.

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                                                                                                       RESULT 4
AAS69866/c
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                                                                                                                                                 The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                  polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                     Sequence 2016 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 5670; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000;
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     39
                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
   AGACATGTGCCAGGAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n; chromosome mapping; gene mapping; gene therapy; forensic;
supplement; medical imaging; diagnostic; genetic disorder;
                                    l Similarity
19; Conserv
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2000US-0649167
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Matches Query Match Best Local

Similarity

4.7%;

Score 19; Pred. No.

DB 23; 15;

Length 2020; Indels

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Gaps

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Conservative

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13

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RESULT 5
AAS82153
                                                                                               The invention relates to isolated polynucleotide (I) and C polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful in generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating cisorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cannot acid sequences. AAS64197-AAS94564 represent novel human collagoration, but was obtained in electronic format directly from WIPO as ferrification, but was obtained in electronic format directly from WIPO as ferrification, but was obtained in electronic format directly from WIPO as ferrification, but was obtained in electronic format directly from WIPO as ferrification.
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 17957; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, us diagnostics, forensics, gene mapping, identification of responsible for genetic disorders or other traits and to biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-639362/73.
P-PSDB; ABG17966.
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23-AUG-2000; 2000US-0649167.
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food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding novel human diagnostic protein #17957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-2002
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                                                                            at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US08631
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       2020
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       BP; 439
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   A; 610 C;
   634 G;
       337 T; 0 other;
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RESULT 7
AAC99130
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DT 09-P
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Best Local
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                                                                                                                                                                                                                                                                      The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, activin/inhibin activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides encoding human secreted proteins - dee.g. human blood, kidney, foetal lung, placenta, testes, ovary, pituitary, retina and colon cDNA libraries.
                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 386; 618pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agostino MJ, Jacobs K, Racie LA, Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy;
Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:358
                           09-MAR-2001
                                                     AAC99130;
                                                                             AAC99130 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEMY ) GENETICS INST INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted protein; expressed sequence tag; EST; haematopoiesis;
tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;
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                                                                                                                                             GAGAAGGAAAGGAGA 300
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                        (first entry)
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                                                                                                                                                                                                                                                A; 79 C;
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Treacy M;
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RESULT 8
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Best Local
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                                                                                             AAH06889 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens have cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 780; 1379pp; English
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                                                 дан06889;
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in gene therapy. The polynucleotide and proteins can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gynaecological, cardiant and antiinflammatory activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen
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                                                                                                                                                                                                                                                                         134 GAGAAGAAGGAAAGGAGA 151
                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                          GAGAAGAAGGAAAGGAGA
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                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or for use in assays for diagnosing a pathological condition
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                                                                                                                                                                                                                                                                                                                                                                                                                           872 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                           253 A; 186 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the exemplification
                                                                                                  cDNA; 899
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Pred. No.
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26-JUN-2001

(first entry)

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RESULT 9
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AC AAA5
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                                                                                                                                                                                                                                                                                                                                                                                                                        of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the polynucleotide comprises a 1'-end sequence, where the polynucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence)3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                 in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                 AAA51824;
                                                                                                                                                                                                                                                                                    represent oligonucleotides, of the present invention
                                               AAA51824 standard;
                                                                                                                                                                                                                                                       Sequence 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention full-length cDNAs defi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
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11-JAN-2000;
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                                                                                                                             742
                                                                                                                                            134 GAGAAGAAGGAAAGGAGA 151
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                                                                                                                                                                                                        Similarity
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                       BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID 3724; 2537pp + CD ROM;
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                                                                                                                                                                                                                                                     246 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tion describes primer sets for synthesising defined in the specification. Where a prime
                                               cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                        4.5%;
                                                                                                                                                                                                                                                     205 C;
                                                1149
                                                                                                                                                                                         0;
                                                                                                                                                                                                                        Score 18;
                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                       265
                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashi K, ;
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ID
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                                                                                                                                                                                                         No.
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                                                                                                                                                                                                                                                    179 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                         48;
                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saito K, Y. Otsuki T;
                                                                                                                                                                                         0;
                                                                                                                                                                                                                        Length 899;
                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a combination
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                                                                                                                                                                                         Gaps
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AAH14264/c
ID AAH142
XX
AC AAH142
AC AAH142
AC 26-JUN
XX
DT 26-JUN
XX
KW Human
XX
KW Human
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                                                                                                                                                RESULT
                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                The invention concerns novel splice variants of the melanocortin 1 receptor (MC-RI) protein belonging to the rhodopsin sub-family of G-protein coupled receptors. The splice variants, referred to as MC-RIB proteins, contain an intracellular domain with an additional 65 amino acid residues in comparison to previously disclosed human MC-RI, referred to as MC-RIA. Additionally, residue 317 of the MC-RIB proteins is Cys, whereas the C-terminal amino acid residue 317 of known MC-RIA proteins is Trp. The novel sequences can be used to determine whether a substance modulates MC-RIB receptor activity and to identify potential agonists or antagonists of MC-RIB are used to treat or diagnose disorders involving inappropriate melanocortin expression or activity.
                                                                                                                                                                                        1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding a human melanocortin 1 receptor protein (MC-R1B) for determining whether a substance is capable of binding to or activating human MC-R1B and identifying a substance that modulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JAN-2001
                                                                                             AAH14264;
                                                                                                                       AAH14264 standard;
                                                                                                                                                                                                                                                                                           Sequence 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 73; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200039147-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modulator; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MC-R1; melanocortin 1 receptor; rhodopsin; G-protein coupled recep splice variant; MC-R1B; C-terminal extension; agonist; antagonist;
                                                                   26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MC-R1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human melanocortin 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MERI ) MERCK & CO INC
                                                                                                                                                                                                               48 CCAGGAGAAGGGCCTTG
                                                                                                                                                                                     CCAGGAGAAGGGGCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-452365/39
DB; AAY97019.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor activity
                                                                                                                                                                                                                                        18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AD, MacNeil DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                  (first entry)
                                                                                                                                                                                                                                                                                             B₽;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US29963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1..1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= Melanocortin_1_receptor_B_splice_variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                             188
                                                                                                                     cDNA; 1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor protein MC-R1ESTc11 cDNA
                                                                                                                                                                                                                                                                                           A; 402
                                                                                                                                                                                                                                                                    4.5%;
                                                                                                                                                                                        1049
                                                                                                                                                                                                                65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Van
                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                       Score 18;
Pred. No.
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                                                                                                                                                                                                                                                                                             319
                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                             G;
                                                                                                                                                                                                                                                     DB
48;
                                                                                                                                                                                                                                                                                            240 T; 0
                                                                                                                                                                                                                                                                    21;
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                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                    Length 1149;
                                                                                                                                                                                                                                                                                             other;
                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                          Gaps
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Human cDNA sequence SEQ ID NO:11581.

Human; primer;

detection; diagnosis; antisense therapy; gene therapy;

SS

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RESULT 11
AAC69571/c
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   XX EXTX XXX II
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Best Local S
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                        in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH3639 represent human amino acid sequences; AAB92446 to AAH3639 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 7-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5-end sequence/3-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-FEB-2001
                              Human secreted protein gene 60 clone HMSGK61.
                                                             31-JAN-2001
                                                                                            AAC69571;
                                                                                                                       AAC69571 standard;
                                                                                                                                                                                                                                                                                                                            Sequence 1205 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HELI-)
                                                                                                                                                                                                      599
                                                                                                                                                                                                                                48 CCAGGAGAAGGGGCCTTG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-318749/34.
                                                                                                                                                                                                   CCAGGAGAAGGGGCCTTG
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                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention describes
                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                           313 A; 283 C;
                                                                                                                         DNA; 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                               4.5%;
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                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                              Score 18;
                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                              309
                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                            300
                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                              22;
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                                                                                                                                                                                                                                                                                            Length 1205;
                                                                                                                                                                                                                                                                                                                            other;
                                                                                                                                                                                                                                                                Indels
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RESULT 12 AAS73815

AAS73815

standard; cDNA; 3099

밁 Q

1090

134 GAGAAGAAGGAAAGGAGA 151 GAGAAGAAGGAAAGGAGA 1073

Conservative

0,

Mismatches

0

Indels

0;

Gaps

0

13-FEB-2002

(first entry)

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss

DNA encoding novel human diagnostic protein #9619

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The invention relates to the isolation of genes (AAC69512-C69587)
CC encoding 62 human secreted proteins (ABB8221-B8396). The genes can be used to generate fusion proteins by linking to the gene for the human cu immunoglobulin G Fc portion (AAC69503) for increasing the stability of the fusion protein as compared to the human protein only. The genes and corotions are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated conditions, e.g. by protein or gene therapy. The genes are isolated conditions, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) autoimmune diseases e.g. the diagnosis, treatment and prevention of: (a) autoimmune diseases e.g. crimematoid arthritis; (b) hyperproliferative disorders e.g. neoplasms cof the breast or liver; (c) cardiovascular disorders e.g. cardiac carest; (d) cerebrovascular disorders e.g. crebral ischemia; (e) cardiovascular disorders e.g. Alzheimer's disease; (g) cardiovascular disorders e.g. Alzheimer's disease; (g) caid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for any cardior contract of the company of the company of the company of the prevent skin aging the company of the company of the prevent skin aging the company of th
Query Match
Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecules encoding 62 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-APR-1999;
26-APR-1999;
                                                                                                                                                        Sequence 1984 BP; 422 A; 512 C; 440
                                                                                                                                                                                                                                             chemotaxis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-647418/62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-APR-2000; 2000WO-US08979.
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99US-0130991.
                                                                                                                                                                                                                                                                             culture
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HS, Ebner
                                    4.5%;
100.0%;
                                                                                                                                                                                                                                                                             of
                                                                                                                                                                                                                                                                             primary tissues, to
                                        Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GA,
R,
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Florence KA,
                                                                                                                                                        G;
                                                                                                                                                        610 T;
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47;
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Moore PA,
                                                                                                                                                                                                                                                                         regenerate tissues
                                                                                Length 1984;
                                                                                                                                                            other;
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Birse
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RESULT 13
AAS84712
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                                                                                                                                                                                                                                                                                                                                                                                                                             CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymucleotides are also used in diagnostics as expressed sequence tags (C polymucleotides are also used in diagnostics as expressed sequence tags (C for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful in generating antibodies against it, detecting or (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical climaging of sites expressing (II). (I) and (II) are useful for treating CC imaging of sites expressing (II). (I) and (II) are useful in medical climaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations (C and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed content of the common of the coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible or genetic disorders or other traits and to assess blockers.
                                                                                                                                                                                             AAS84712 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 9619; 103pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000;
23-AUG-2000;
                                  Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                    DNA encoding novel human diagnostic protein #20516
                                                                                                                           13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001; 2001WO-US08631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide (II) sequences.
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                                                                                                                                                                                                                                                                                                                      134 GAGAAGAAGGAAAGGAGA 151
                                                                                                                                                                                                                                                                                     724
                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                     GAGAAGAAGGAAAGGAGA 741
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                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                           Conservative
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2000US-0649167.
                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           BP; 881 A; 794 C; 818 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   relates to isolated
                                                                                                                                                                                              cDNA; 3099
                                                                                                                                                                                                                                                                                                                                                                       4.5%;
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Pred. No.
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s useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                             606 T; 0 other;
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47;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printer specification, but was obtained in electronic format directly from WI at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                             DNA encoding
                                                                                                                                                                                                                AAS72090 standard; cDNA; 3137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymerase chain reaction (PCR) primers, oligomers, and for and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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23-AUG-2000;
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                             Homo sapiens
                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                              13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3099 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 20516; 103pp; English.
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ypeptide (II) sequences. (I) is useful as hybridisation probes.
                                                                                                                                                                                                                                                                                                  GAGAAGAAGGAAAGGAGA 741
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2000US-0649167
                                                                                                               novel human
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                                                                                                               diagnostic protein #7894
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Pred. No.
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47;
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from WIPO
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RESULT 15
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Best Local
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                                                                                                                                                                                                                                               Human;
                                                                                                                                                                                                                                                                                                                 Human cDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-639362/73.
P-PSDB; ABG07903.
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23-AUG-2000;
                                 07-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH14592 standard; cDNA; 3288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001;
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                                                                                                                                                                                                                                           primer;
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2000US-0649167.
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                                                                                                                                                                                                                                        detection; diagnosis; antisense therapy; gene therapy; ss.
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100.0%;
                                                                                                                                                                                                                                                                                                                 SEQ ID NO:12199.
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47;
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Search completed: January Job time: 363 secs

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GAGAAGAAGGAAAGGAGA

759

134 GAGAAGAAGGAAAGGAGA 151

Matches

Conservative

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Mismatches

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to the 5602 nucleotide sequences defined in the specification, where the complementary strand of a polynucleotide which comprises one of coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary to a combination of complementary to a complementary to a complementary to a complementary to a coligonucleotide which comprises a 3'-end sequence complementary to a coligonucleotide comprises a 3'-end sequence, where the coligonucleotide comprises a 1'-end sequence, where the coligonucleotide comprises as a selected from those defined in comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in comprises are useful for synthesising polynucleotides, are therapy. The primers are useful for synthesising polynucleotides, carticularly full-length cDNAs. The primers are also useful for the comprise and coligonucleotides of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs and coligonucleotides, and AAH13613 to AAH13628 and can be comprised to AAH13628 and coligonucleotides, all of which are used in the exemplification of the present invention.
                 Query Match
Best Local
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; SEQ ID 12199; 2537pp + CD ROM; English
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                                                                         Sequence
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l Similarity
18; Conserv
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Sugiyama T, Wakamatsu
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                         945 A; 768 C;
               4.5%;
                 Score 18;
Pred. No.
                                                                         882 G;
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A, Nagai K,
                   No.
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Maximum DB
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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,
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Match Length DB
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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1 US-08-081-661-16
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1 US-08-081-661-16
1 US-08-081-661-16
1 US-08-948-128
4 US-08-94-962-14
5 PCT-US-95-085-96-1
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Sequence 19, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 18, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	13	•	Sequence 11, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 11, Appl	Trader / , contraction

## ALIGNMENTS

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RESULT 1

US-09-134-001C-66

US-09-134-001C-66

Sequence 66, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

FITTLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO S

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-10-08

PRIOR FILING DATE: 1997-08-14

PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-09-134-001C-1790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-66
                                                                                   GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
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SEQ ID NO 66
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1790
LENGTH: 597
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                      Sequence 1790, Application US/09134001C Patent No. 6380370
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Best Local :
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US-09-737-698B-11/c
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APPLICANT: Fincher, Karen
APPLICANT: Wilkinson, Jack
APPLICANT: Wilkinson, Jack
TITLE OF INVENTION: No. 6462258el Plant Expression Constructs
FILE REFERENCE: 38-21(51499)C
CURRENT APPLICATION NUMBER: US/09/737,698B
CURRENT FILING DATE: 2000-12-15
CURRENT FILING DATE: 2000-12-15
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application PC/TUS9206532
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
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Best Local Similarity 100.0%;
Matches 17; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/171,173 PRIOR FILING DATE: 1999-12-16
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OTHER INFORMATION: Actl1 promoter polynucleotide segeunce and
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TYPE: DNA
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25,275
REGISTRATION NUMBER: 07-24(776)A
                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Human Substance P Receptor NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SD STREET: 800 N. Lindbergh Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325 TCTGATGCATTCCATTT 341
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                                                                                              APPLICATION NUMBER: POFILING DATE: 19920805
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Pred. No.
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Pred. No.
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                                                                                                                                                                        Sequence 146, Application US/08857946 Patent No. 5994075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.0 SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Fincher, Karen
APPLICANT: Wilkinson, Jack
TITLE OF INVENTION: No. 6462258el Plant Exp
FILE REFERENCE: 38-21(5149)C
CURRENT APPLICATION UNMBER: US/09/737,698B
CURRENT FILING DATE: 2000-12-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (314)694-31
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: promoter LOCATION: (1)..(1946) OTHER INFORMATION: chime OTHER INFORMATION: ntro
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TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                         APPLICANT: Goodfellow, P.N.
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: GENE OF
NUMBER OF SEQUENCES: 162
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                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                      595 TCTGATGCATTCCATTT 579
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                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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COUNTRY:
                                               STREET:
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                Massachusetts
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                                               State
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RESULT 7
US-08-970-740-146
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Best Local Similarity
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/017,824
FILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kathleen M. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
                                                                       APPLICATION NUMBER: 08/857,946 FILING DATE: 16-MAY-1997 PRIOR APPLICATION DATA:
                                                                                                                    APPLICATION NUMBER: 14-NOV-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: METHODS FOR IDENTIFYING A MUTATION IN TITLE OF INVENTION: GENE OF INTEREST NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 617-345-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                         APPLICATION NUMBER: 60/01 FILING DATE: 17-MAY-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Goodfellow, P.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER:
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28 State Street, 28th Flo
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14-NOV-1997
ON DATE:
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Query Match
Best Local Similarity
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; MOLECULE TYPE:
US-07-918-953-3
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                                                    Query Match
Best Local S
Matches 16
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                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/918,953
FILING DATE: 19920730
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 617-227-7111
TELEFAX: 617-227-4399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ANDY, ROBIN J. APPLICANT: LARSON, ERIC R. TITLE OF INVENTION: TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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STREET: /J
CITY: PALO ALTO
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                          191 TCCAGGGCCAAGGGCT 206
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TELEPHONE: 415) 494-0792
92 TCCAGGGCCAAGGGCT
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linear
E: DNA
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100.0%; Pred. No.
                                                                4.0%; Score 16;
100.0%; Pred. No.
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US-08-081-661-3/c
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                                                                                                                                                                                                                 Sequence 32, Application US/08487001A Patent No. 5795862 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 219(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-677-7000
TELEFAX: (415) 494-0792
TELEX: 706141
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                 APPLICANT: FRANK, GLENN R.

APPLICANT: HUNTER, SHIRLEY WU

APPLICANT: WALLENGELS, LYNDA

TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA

TITLE OF INVENTION: PROTEINS AND APPARATUS TO COLLECT SUCH PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 99 base pairs
TYPE: nucleic acid
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PRIOR APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 15
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 30-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, KARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ANDY, ROBIN J.
APPLICANT: LARSON, ERIC R.
TITLE OF INVENTION: TISSUE-SELECTIVE INSULIN ANALOGS
                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                         NUMBER OF SEQUENCES:
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                                     CITY:
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COUNTRY:
                                                    STREET:
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                                                   1700 Lincoln Street, Suite 3500
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                                                                    Sheridan Ross & McIntosh
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100.0%; Pred. No. 38
Live 0; Mismatches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (303) 863-02
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FRANK, SHIRLEY WU
APPLICANT: HUNTER, SHIRLEY WU
APPLICANT: WALLENFELS, LYNDA
APPLICANT: NUENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
AND APPARATUS TO COLLECT SUCH PROTEINS
                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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         TELEPHONE: (303)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 AATTATTGCTCAGATG 144
                                                                                                                                         APPLICATION NUMBER: US/08 FILING DATE: 11-APR-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 80203
                                                                                                                                                                                                                                                                                                                                                    CITY: Denver
STATE: Colora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 AATTATTGCTCAGATG 102
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LOCATION: 3...
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                    Colorado
                                                                                                                                                                                                                                                                                                                                                                                      1700 Lincoln Street, Suite 3500
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             863-0223
                                                                                                                                                                                 US/08/630,822A
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                                                                                    32,020
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                                                                      2618-17-C3
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RESULT 12
US-09-005-069-32
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               Query Match
Best Local Similarity
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    Matches
                                                                                                                                                                                                      TELEFAX: (303) 863-0223 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FRANK, GLENN R.

APPLICANT: HUNTER, SHIRLEY WU

APPLICANT: WALLENFELS, LYNDA

TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS

TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 242 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/63
FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GARY J
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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LENGTH: 242 base pairs
                                                                                                       FEATURE:
                                                                                                                 MOLECULE TYPE:
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                                                                        NAME/KEY:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 AATTATTGCTCAGATG 102
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STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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               4.0%; Score 16;
100.0%; Pred. No.
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   Mismatches
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39;
               DB 2;
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                            Length 242;
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Gaps
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; NAME/KEY: CDS
; LOCATION: 209..271
; OTHER INFORMATION: 1
; OTHER INFORMATION: 1
; OTHER INFORMATION: A
US-07-918-953-12
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US-07-918-953-14/c
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US-07-918-953-12/c
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                            Patent No. 5268453
GENERAL INFORMATION:
                                                                                                                              Sequence 14, Application US/07918953 Patent No. 5268453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/07918953 Patent No. 5268453
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/918,953
FILING DATE: 19920730
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DOTICETION
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             APPLICANT: ANDY, ROBIN J.
APPLICANT: LARSON, ERIC R.
TITLE OF INVENTION: TISSUE-SELECTIVE INSULIN ANALOGS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-677-7000
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 275 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ANDY, ROBIN J.
APPLICANT: LARSON, ERIC R.
APPLICANT: LARSON: TISSUE-SELECTIVE INSULIN ANALOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                               189 TCCAGGGCCAAGGGCT 174
                                                                                                                                                                                                                                                                                  191 TCCAGGGCCAAGGGCT 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: BOZICEVIC, KARL
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MORRISON & FOERSTER
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                                                                                                                                                                                                                                                                                                                                                                                                                 A chain."
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is numbered from amino acid number 1 of the
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STREET: // CITY: PALO ALTO STATE: CALIFORNIA

755 PAGE MILL ROAD

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RESULT 15
US-08-081-661-12/c
; Sequence 12, Application US/08081661
; Patent No. 5446020
; GENERAL INFORMATION:
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TELEPHONE: 415-677-7000
TELEFAX: (415) 494-0792
TELEFAX: 705141
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 275 base pairs
TYPB: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,661
FILING DATE: 23-UN-1993
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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ZIP: 94304-1018
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                               STREET: /J.
STREET: /J.
STREET: /J.
STREET: /J.
STATE: CALIFORNIA
MSA
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ANDY, ROBIG J.
APPLICANT: LARSON, ERIC R.
TITLE OF INVENTION: TISSUE-SELECTIVE INSULIN ANALOGS
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, KARL
REGISTRATION NUMBER: 28,807
                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 209..271
OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: cDNA
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189 TCCAGGGCCAAGGGCT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: U: FILING DATE: 19920730 CLASSIFICATION: 514
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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LOCATION: 209
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                                                                                                                                                                                                                                                                                              755 PAGE MILL ROAD
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is numbered from amino acid number 1 of the
A chain."
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US 07/918,953
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Pred. No.
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Search completed: January 2, 2003, 16:01:03 
Job time: 78 secs
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TELLEX: 706141
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 275 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                   Matches
                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             NAME: BOZICEVIC, KARL

REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 21900-2027420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-677-7000
TELEPAX: 415,494-0792
TELEFAX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 30-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, KARL
                                                            189
                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 209..271
COTHER INFORMATION: J
OTHER INFORMATION: J
OTHER INFORMATION: J
                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                    TOPOLOGY: 1:
                                                                                      191 TCCAGGGCCAAGGGCT 206
                                                          TCCAGGGCCAAGGGCT
                                                                                                                   16;
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                     CDNA
                                                                                                                                 4.0%;
                                                                                                                                                                                          /note= "The insulin analog is numbered from amino acid number 1 of the A chain."
                                                            174
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                                                                                                                                Score 16;
; Pred. No.
                                                                                                                   0;
                                                                                                                   Mismatches
                                                                                                                                   DB 1;
39;
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                                                                                                                   Indels
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0

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Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  January 2, 2003, 16:01:07 ; Search time 84 Seconds (without alignments) 2069.842 Million cell updates/sec
         402
1 ccgggccgggctcaccagct.....ggcataacttcctgtgttcc 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381593 seqs, 216252194 residues
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:/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US08_DUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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:/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

19	18	c 17	c 16	c 15	c 14	c 13	c 12	c 11	10	9	c 8	c 7	с 6	ი 5	4	с 3	2	1	Result
17	17	17	17	17	17	17	17	17	17	17	18	18	18	18	18	18	18	22	Score
4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	<b>4</b> .5	4.5	4.5	4.5	4.5	4.5	4.5	5.5	Query Match
3597	2982	1946	1393	1183	1183	498	260	219	179	179	25279	25279	25277	25277	4623	2000	872	574	Length
9	9	10	10	10	9	10	10	9	10	10	10	10	10	10	10	9	10	12	DB
US-10-098-841-84	US-09-938-842A-398	US-09-737-626A-27	US-09-737-626A-11	US-09-443-704-33	US-10-008-118A-33	US-09-925-297-346	US-09-878-574-11983	US-09-796-692-7632	US-09-880-107-2996	US-09-954-456-1496	US-09-764-860-1147	US-09-764-878-284	US-09-764-860-1148	US-09-764-878-285	US-09-864-864-288	US-09-938-842A-3855	US-09-925-297-358	US-10-062-254-335	ID
Sequence 84, Appl	Sequence 398, App	Sequence 27, Appl		Sequence 33, Appl	Sequence 33, Appl	Sequence 346, App	Sequence 11983, A	Sequence 7632, Ap	Sequence 2996, Ap	Sequence 1496, Ap	Sequence 1147, Ap	284,	Sequence 1148, Ap	•	Sequence 288, App	•	Sequence 358, App	Sequence 335, App	Description
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10	10	10	9	10	9	9	10	9	10	10	10	10	10	ဖ	10	9	10	10	7	10	10	10	10	
US-09-864-761-9876	US-09-864-761-68//	US-09-899-917-11	US-09-728-444-427	US-09-867-550-1781	US-09-796-692-9012	US-09-796-692-4911	US-09-899-917-12	US-09-804-409A-10	US-09-783-590-8704	US-09-864-761-10796	US-09-960-352-10581	US-09-280-030-48	US-09-864-761-14179	US-09-938-842A-4736	US-09-280-030-49	US-09-796-692-7386	US-09-899-917-14	US-09-878-574-7917	US-08-809-423A-32	US-09-867-701-7968	US-09-789-529-20	US-09-974-300-5722	US-09-563-817-655	(C (C) (C) (C) (C) (C) (C) (C) (C) (C) (
Sequence 9876, Ap	sequence b8//, Ap	Sequence 11, Appl	Sequence 427, App	Sequence 1781, Ap	Sequence 9012, Ap	Sequence 4911, Ap	Sequence 12, Appl	Sequence 10, Appl	Sequence 8704, Ap	Sequence 10796, A	Sequence 10581, A	Sequence 48, Appl	Sequence 14179, A	O	Sequence 49, Appl	Sequence 7386, Ap	Sequence 14, Appl	Sequence 7917, Ap	Sequence 32, Appl	Sequence 7968, Ap	Sequence 20, Appl	Sequence 5722, Ap	Sequence 655, App	004000000000000000000000000000000000000

## ALIGNMENTS

; PRIOR FILING DATE: 1999-12-21 ; PRIOR APPLICATION NUMBER: 600/171515 ; PRIOR FILING DATE: 1999-12-22	 APPLICATION	 ) PRIOR FILING DATE: 1999-10-01 - DRIOR ADDITIONTON UNIMAREP - 60/169767	 PRIOR FILLING DATE: 1999-09-30	PILING DATE	APPLICATION I	FILING DATE: 1999-0	PRIOR ADDITICATION NUMBER: 60/146511	; CURRENT FILING DATE: 2002-02-01	CURRENT APPLICATION NUMBER: US/10/062,254	111000111111111111111111111111111111111	: TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism	••	 ••	••	; APPLICANT: Niu, Xiping	 ••	••	••	: Fang,	Falco, Saverio C	APPLICANT: Cahoon, Rebecca E	; GENERAL INFORMATION:	; Patent No. US20020138882A1	RESULT 1 US-10-062-254-335
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RESULT 3
US-09-938-842A-3855/c
; Sequence 3855, Application US/09938842A
; Patent No. US20020160378A1
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NAME/KEY: misc feature

LOCATION: (803)

OTHER INFORMATION: n equals a,t,g, or

NAME/KEY: misc feature

LOCATION: (813)

OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                     Matches
                                                                                                                                                                                                     Query Match
Best Local :
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SEQ ID NO 358
LENGTH: 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Microsoft Office 97
SEQ ID NO 335
LENGTH: 574
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR PPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
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LOCATION: (495)
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PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: PA105
                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature LOCATION: (871)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: unsure LOCATION: (538)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                                                                   134 GAGAAGAAGGAAAGGAGA 151
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                                                                                                                                                                                   Local Similarity 100.0%;
nes 18; Conservative (
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100.0%; Pred. No.
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0; Mismatches
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0.046;
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2000-01-06-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEG ID NOS: 5379
SEQ ID NO 3855
LENGTH: 2000
                                                Query Match
Best Local Similarity
Watches 18; Conserva
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                                                                                                                                         ; ORGANISM: Homo sapiens US-09-864-864-288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.5%; Score 18; Best Local Similarity 100.0%; Pred. No. Matches 18; Conservative 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                   APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.523
CURRENT APPLICATION NUMBER: US/09/864,864
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Harper, Jeff APPLICANT: Kreps, Joel
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                                                                                                                                                                           LENGTH: 4623
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Arabidopsis thaliana
1072 GAGAAGAAGGAAAGGAGA 1089
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                                 134 GAGAAGAAGGAAAGGAGA 151
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o. US20020102679A1
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Zhu, Tong
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Benson, Darin R.
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Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lodes, Michael J.
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                                                                    Conservative
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                                                                                     4.5%; Score 18;
100.0%; Pred. No.
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7.3;
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RESULT 5 US-09-764-878-285/c ; Sequence 285, Application US/09764878

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US-09-764-860-1148/c; Sequence 1148, Application US/09764860; Patent No. US20020094953A1
                                                                                                                                                                                                                                                                                                        US-09-764-878-284/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LENGTH: 25277
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-1148
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                                  ; TYPE: DNA; ORGANISM: Homo sapiens US-09-764-878-284
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                                                                                   SOFTWARE: PatentIn Ver.
SEQ ID NO 284
LENGTH: 25279
                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           Sequence 284, Application US/09764878 Patent No. US20020090615A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1148
LENGTH: 25277
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SEQ ID NO 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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 Query Match
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                                                                                                                                                                                                   APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PC008
                                                                                                                                  Prior application data removed - consult PALM or NUMBER OF SEQ ID NOS: 428
                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/764,878
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/764,860 CURRENT FILING DATE: 2001-01-17
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CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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TYPE: DNA
ORGANISM: Homo sapiens
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100.0%; Pr
100.0%; 0;
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4.5%;
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Pred. No.
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Pred. No.
Score 18;
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DB 10;
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Length 25279;
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RESULT 8
US-09-764-860-1147/c
US-09-764-860-1147, Application US/09764860
; Patent No. US20020094953A1
; Patent No. US20020094953A1
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                                          NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn ve.
SEQ ID NO 1496
LENGTH: 179
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Matches 18; Conserv
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PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR EILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
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CURRENT FILING DATE: 2001-09-18
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                                                                                                                            PRIOR FILING DATE:
                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/60/235,840 PRIOR FILING DATE: 2000-09-27
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PRIOR APPLICATION NUMBER: US/60/235,720
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                                                                                                                                                    PRIOR APPLICATION NUMBER: US/60/235,863
ORGANISM: Homo sapiens
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RESULT 11
US-09-796-692-7632/c
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US-09-880-107-2996
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CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,303
                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
                                                                                                                                                                                                                                                                                                                        Sequence 7632, Application US/09796692 Publication No. US20020198362A1
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SEQ ID NO 2996
LENGTH: 179
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Patent No. US20020142981A1
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Best Local :
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CURRENT FILLING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
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TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
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APPLICANT: Vockle
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NAME/KEY: misc_feature
OTHER INFORMATION: n=a,t,g
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US-09-796-692-7632
                                                                   US-09-878-574-11983
                                                                                                                                                             APPLICANT: La Rosa, Thomas J.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and Ot)

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(15401)B

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR FILING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 15775
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Best Local S
Matches 17
                                                                               SEQ ID NO 11983
LENGTH: 260
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701065166H1
Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                              Sequence 11983, Application US/09878574 Patent No. US20020110548A1
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OTHER INFORMATION: r
NAME/KEY: unsure
LOCATION: (187)
OTHER INFORMATION: r
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SOFTWARE: FastSEQ for Windows Version
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PRIOR FILING DATE: 2000-08-07
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TYPE: DNA
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APPLICATION NUMBER: 60/218,950
FILING DATE: 2000-07-14
APPLICATION NUMBER: 60/222,903
FILING DATE: 2000-08-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/200,999
FILING DATE: 2000-05-01
APPLICATION NUMBER: 60/202,084
FILING DATE: 2000-05-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/206,201
4.2%; Score 17; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
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; LOCATION: (252)
; OTHER INFORMATION: n equals a,t,g, or
; NAME/KEY: misc feature
; LOCATION: (493)
; OTHER INFORMATION: n equals a,t,g, or
US-09-925-297-346
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US-09-925-297-346/c
                                                                                                                                         US-10-008-118A-33
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                                                                                                                                                                                       TITLE OF INVENTION: Plant MYB-Related Transcription Factors
FILE REFERENCE: BB1280 USDIV
CURRENT APPLICATION NUMBER: US/10/008,118A
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/109,294
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Office 97
SEQ ID NO 33
LENGTH: 1183
                                                                                       Best
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PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cahoon, Rebecca E. APPLICANT: Weng, Zude
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CURRENT FILING DATE: 2001-08-10
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
                                                                                                                                                        TYPE: DNA ORGANISM: Triticum aestivum
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ORGANISM: Homo sapiens
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1089 AAGAAGGAAAGGAGATG 1073
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; ORGANISM: Triticum aestivum
US-09-443-704-33
Search completed: January 2, 2003, 17:49:29 Job time: 134 secs
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US-09-443-704-33/c
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Best Local
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LENGTH: 1183
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CURRENT FILING DATE: 1999-11-19
EARLIER APPLICATION NUMBER: 60/109,294
EARLIER FILING DATE: NO. US20020066120Alember 20, 1998
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cahoon, Rebecca E.
APPLICANT: Liu, Zhan-Bin
APPLICANT: Odell, Joan
APPLICANT: Rafalski, Antoni
APPLICANT: Shi, June
APPLICANT: Weng, Zude
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant MYB-Related Transcription Factors
FILE REFERENCE: BB1280 US NA
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| cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
| cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
| cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
| cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
| cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
| cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
| cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
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2271.753 Million cell updates/sec
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US-09-539-335D-1
US-09-534-850-20438
US-09-513-999C-20190
US-09-513-999C-31199
US-09-513-999C-31199
US-09-513-999C-31198
US-10-092-411A-1790
US-09-724-676-25006
US-09-724-676A-25006
US-09-724-676A-25006
US-09-724-676A-25008
US-09-724-676A-25009
US-09-724-676A-25009
US-09-724-676A-25009
US-09-724-676A-25009
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US-09-539-333D-1
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ALIGNMENTS	US-10-229-834A-6	US-09-724-676A-23591	US-09-724-676-23591	US-09-724-676A-24990	US-09-724-676-24990	US-09-724-676A-24995	US-09-724-676-24995	US-09-724-676A-24988	US-09-724-676-24988	US-09-724-676A-24993	US-09-724-676-24993	US-09-724-676A-24989	US-09-724-676-24989	US-09-724-676A-24987	US-09-724-676-24987	US-09-724-676A-24994	US-09-724-676-24994	US-09-724-676A-24992	US-09-724-676-24992
	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
	6, Appli	23591, A	23591, A	24990, A	24990, A	24995, A	24995, A	24988, A	24988, A	24993, A	24993, A	24989, A	24989, A	24987, A	24987, A	24994, A	24994, A	24992, A	24992, A

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RESULT 1

US-10-310-188-10261/c

US-10-310-188-10261/c

Sequence 10261, Application US/10310188

GENERAL INFORMATION:

APPLICANT: ROSEKTAGEMODICS

TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROTITLE OF INVENTION: USES THEREOF

FILE REFERENCE: 47487

CURRENT APPLICATION NUMBER: US/10/310,188

CURRENT FILING DATE: 2002-12-19

NUMBER OF SEQ ID NOS: 86841
APPLICANT: ESSION, Laurent
TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PRO
FILE REFERENCE: GENSEF: 047AUS
CURRENT APPLICATION NUMBER: US/09/539,333D
CURRENT FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: US 60/126,903
PRIOR FILING DATE: 1999-03-90
PRIOR PRIOR APPLICATION NUMBER: US 60/131,971
PRIOR APPLICATION NUMBER: US 60/132,065
PRIOR APPLICATION NUMBER: US 60/132,065
PRIOR APPLICATION NUMBER: US 60/132,065
PRIOR APPLICATION NUMBER: US 60/143,928
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 60/143,928
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 60/145,915
                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Me
APPLICANT: Chunakov, ilye
APPLICANT: Bougueleret, I
APPLICANT: Bihain, Bernar
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-10261
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Best Local Similarity 100.0%;
Matches 18; Conservative
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Chumakov, Ilya
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PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: US 60/146,453
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 60/146,452
PRIOR FILING DATE: 1999-07-29
PRIOR PELICATION NUMBER: US 60/162,288
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 09/416,384
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 231
SOFTWARE: Patent.pm
                                                                                                                                                FEATURE:
NAME/KEY: allele
LOCATION: 129789
OTHER INFORMATION: I
                                                                         NAME/KEY: allele
LOCATION: 130777
OTHER INFORMATION: FEATURE:
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NAME/KEY: allele
LOCATION: 126105
OTHER INFORMATION:
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NAME/KEY: allele
LOCATION: 121527
OTHER INFORMATION: F
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NAME/KEY: allele
LOCATION: 112468
OTHER INFORMATION: £
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NAME/KEY: allele
LOCATION: 120573
OTHER INFORMATION: I
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NAME/KEY: allele
LOCATION: 119526
OTHER INFORMATION: |
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NAME/KEY: allele
LOCATION: 118972
OTHER INFORMATION: 1
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NAME/KEY: allele
LOCATION: 110222
OTHER INFORMATION: polymorphic base G
                             NAME/KEY: allele
LOCATION: 136942..136944
OTHER INFORMATION: delet
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NAME/KEY: allele
LOCATION: 117324..117327
OTHER INFORMATION: deletion ACTT
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LOCATION: 111978
OTHER INFORMATION:
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LOCATION: 119321
OTHER INFORMATION:
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LOCATION: 119316
OTHER INFORMATION:
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LOCATION: 119160..119161
OTHER INFORMATION: deletion
NAME/KEY: allele
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NAME/KEY: allele LOCATION: 154502	HCM	NAME/KEY: allele LOCATION: 153925 OTHER INFORMATION: po			NAME/KEY: allele LOCATION: 152766 OTHER INFORMATION: po	Y: allele N: 152691 NFORMATION:	RIO	NAME/KEY: allele LOCATION: 151769 OTHER INFORMATION: po	Y: allele N: 151748 NFORMATION: d	NAME/KEY: allele LOCATION: 151637 OTHER INFORMATION: po	NAME/KE: allele LOCATION: 149113 OTHER INFORMATION: po	RIOKE	ME/KE ME/KE CATIO HER I	ME/KEY: allele ME/KEY: allele CATION: 148183 HER INFORMATION: d	HCH	NAME/KEY: allele LOCATION: 147281 OTHER INFORMATION: po	NAME/KEY: allele LOCATION: 146668 OTHER INFORMATION: po	TIO R I
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OTHER INFORMATION:

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Best Local
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PRIOR FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: US 60/131,971
PRIOR FILING DATE: 1999-04-30
                                                                                                                                                                                                                                                                                                               APPLICANT: Cohen, APPLICANT: Blume APPLICANT: Chuma
                                                                                                                                          PRIOR
                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/539,333D CURRENT FILING DATE: 2000-03-30
                                                                                                                                                                                                                                          APPLICANT: ESSIOUX, LAURENT TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS FILE REFERENCE: GENSET.047AUS
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NAME/KEY: allele
LOCATION: 156448
OTHER INFORMATION: F
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LOCATION: 158172
OTHER INFORMATION:
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LOCATION: 157238
OTHER INFORMATION:
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LOCATION: 155802
OTHER INFORMATION:
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LOCATION: 154879
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LOCATION: 154677
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LOCATION: 157897
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                                                                 APPLICATION NUMBER: US 60/132,065 FILING DATE: 1999-04-30 APPLICATION NUMBER: US 60/143,928 FILING DATE: 1999-07-14 APPLICATION NUMBER: US 60/145,915 FILING DATE: 1999-07-27
                                      APPLICATION NUMBER: US 60/146,453
FILING DATE: 1999-07-29
APPLICATION NUMBER: US 60/162,288
              APPLICATION NUMBER: US 60/146,452 FILING DATE: 1999-07-29
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18; Conser
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NUMBER OF SEQ ID NOS: 231
SOFTWARE: Patent.pm
SEQ ID NO 1
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PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 1999-10-12
                                                                                                                                                                                             NAME/KEY: exon
201188..201234
NAME/KEY: misc_feature
LOCATION: 213818..215818
OTHER INFORMATION: 3'regulatory region g34872 gene
                                                NAME/KEY: exon
LOCATION: 216836..216915
OTHER INFORMATION: exon
                                                                                                NAME/KEY: exon
LOCATION: 215702..215746
OTHER INFORMATION: exon '
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LOCATION: 1108..128
OTHER INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                LOCATION: 214676...2
OTHER INFORMATION:
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LOCATION: 65854..67854
OTHER INFORMATION: 3'regulatory region g35018
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LOCATION: 65505..65
OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 14877..14920
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LOCATION: 64666..64812
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LOCATION: 25593..25740
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NAME/KEY: exon
LOCATION: 240528..2
OTHER INFORMATION:
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LOCATION: 240528..240617
OTHER INFORMATION: exon
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LOCATION: 240528...2
OTHER INFORMATION:
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LOCATION: 237406..237428
OTHER INFORMATION: exon
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LOCATION:
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LOCATION: 239719..239853
OTHER INFORMATION: exon I
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LOCATION: 239719...
OTHER INFORMATION:
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LOCATION: 234174..234321
OTHER INFORMATION: exon
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LOCATION: 216661..216952
OTHER INFORMATION: exon
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LOCATION: 231870..231879
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LOCATION: 231787...
OTHER INFORMATION:
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LOCATION: 231272..231412
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LOCATION: 230408...
OTHER INFORMATION:
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OCATION: 240528..240569
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LOCATION: 216661..217061
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OCATION: 217027..217061
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229647..229742
exon X (
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DRMATION: exon M1090
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ORMATION: exon P
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215819..215941
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DRMATION: exon
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215819..215975
                    240528..240644
    exon MS2 complement g34872 gene
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                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 07/916,491
PRIOR FILING DATE: 1992-07-17
PRIOR APPLICATION NUMBER: 07/977,780
PRIOR FILING DATE: 1992-11-19
PRIOR APPLICATION NUMBER: 08/100,523
PRIOR FILING DATE: 1993-08-03
PRIOR APPLICATION NUMBER: 09/008,119
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-16
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Best Local
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING
FILE REFERENCE: PD-1020 CIP
                                                                                                                                                      PRIOR
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NUMBER
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OTHER INFORMATION: 3'regulatory region g34665
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LOCATION: 241686..243685
OTHER INFORMATION: 5'regulatory
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OTHER INFORMATION:
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                                                                                                                                                                                  APPLICATION NUMBER: 08/196,364
FILING DATE: 1994-02-14
APPLICATION NUMBER: 08/282,991
                                                                                                  FILING DATE: 1995-05-10
APPLICATION NUMBER: 08/179,873
FILING DATE: 1994-01-11
                                   FILING DATE: 1993-10-1
                                                                                                                                                                        FILING DATE: 1994-07-28
                                                 FILING DATE: 1995-07-20 APPLICATION NUMBER: 08/137,951
                                                                                  APPLICATION NUMBER: 08/504,732
                                                                                                                                                    APPLICATION NUMBER: 08/438,571
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18; Conserv
Prior Application data removed - SEQ ID NOS: 26730
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240528.
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292653..292841
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290652..2926
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240528..241685
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240800..240993
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240528..240824
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Delegeane, Angelo M.
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SOFTWARE: PERL Program

ID NO 21604

ENGTH:

236

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; NAME/KEY: unsure
; LOCATION: 210, 228
; OTHER INFORMATION: a,
US-09-534-850-21604
                                                                           ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00483915
US-09-534-850-20438
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Best Local (
                                       Query Match
                                                                                                                                                                                       Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEO ID NOS: 26730

SOFTWARE: PERL Program
SEO ID NO 20438
LENGTH: 238
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING METABOLIC MOLECULES
FILE REFERENCE: PD-1020 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 07/916,491
PRIOR FILING DATE: 1992-07-17
PRIOR APPLICATION NUMBER: 07/977,780
PRIOR FILING DATE: 1992-11-19
PRIOR FILING DATE: 1992-11-19
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                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1993-10-14
                                                                                                                                       ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                           TYPE: DNA
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OTHER INFORMATION: Incyte
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                   Local
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FILING DATE: 1993-08-03
APPLICATION NUMBER: 09/008,119
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/438,571 FILING DATE: 1995-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/282,991 FILING DATE: 1994-07-28
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17; Conser
th 4.2%; Score 17; DB 5; Length 238; Similarity 100.0%; Pred. No. 34; 17; Conservative 0; Mismatches 0; Indels
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Pred. No.
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; NAME/KEY: misc_feature; LCCATION: 254; OTHER,INFORMATION: r-a or US-09-513-999C-14719
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; LOCATION: 136
; OTHER INFORMATION: y=c or t
US-09-513-999C-20190
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LENGTH: 254
TYPE: DNA
                                                                                                                                                                                                      SOFTWARE: Patent.pm
SEQ ID NO 14719
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CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                           APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags
FILE REFERENCE: 59.US2.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/513,999C CURRENT FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR FILING DATE: 1999-02-26 NUMBER OF SEQ ID NOS: 36681 SOFTMARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
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                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: 133
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                                                                                                                                                                                       ENGTH: 261
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Local Similarity 100. es 17; Conservative
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                 Score 17;
Pred. No.
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Gaps
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RESULT 10
US-10-092-411A-1790
; Sequence 1790, Application US/10092411A
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: MCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
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US-09-513-999C-33198
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Best Local S
Matches 17
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GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TILLE REFERENCE: 032796-101

CURRENT APPLICATION NUMBER: US/10/092,411A

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 09/134,001

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5676
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SEQ ID NO 33198
LENGTH: 324
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                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Staphylococcus epidermidis
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Pred. No.
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; TYPE: DNA; ORGANISM: Homo sapiens US-09-724-676A-25002
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Sequence 25002, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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; TYPE: DNA
; ORGANISM: Staphylococcus
US-10-092-411A-1790
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
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PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5676
SEQ ID NO 1790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.2
SEQ ID NO 25002
LENGTH: 1165
TYPE: DNA
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               Query Match
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Best Local
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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CURRENT APPLICATION NUMBER: US/10/092,411A
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US 09/134,001
PRIOR, FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                              LENGTH: 1165
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               Score 17; pred. No.
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135 AGAAGAAGGAAAGGAGA 151

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RESULT 14

US-09-724-676A-25006/c

Sequence 25006, Application US/09724676A

SEQUENCE INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 25006

LENGTH: 1199

TYPE: DNA

ORGANISM: Homo sapiens

US-09-724-676A-25006
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ITILE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 25006

LENGTH: 1199

TYPE: DNA

ORGANISM: Homo sapiens

US-09-724-676-25006
Sequence 25004, Application US/09724676

GENERAL INFORMATION:
APPLICANT: Compugen LTD
ITILE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 25004
LENGTH: 1203
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-676-25004
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US-09-724-676-25006/c
; Sequence 25006, Application US/09724676
; GENERAL INFORMATION:
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US-09-724-676-25004/c
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Matches 17; Conserva
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BG354266
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EST.
                                       Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                Unpublished (1999)
Contact: Walbot V
                                                                                                 Walbot, V.
Maize ESTs from various
University
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Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
l (bases 1 to 352)
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/organism="Zea mays"
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                                                                                                                                          Embryophyta; Tracheophyta;
a; Poales; Poaceae; PACC
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BG842699 MEST39-A0
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A1978092 614022D04
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AY109457 Zea my5
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BE007187 BB007187 BB007187
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AW946080 QV0-ET000
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BH104961 RPCI-24-2
AZ638587 1M0498L05
AW924010 WS1_32_C0
BQ454260 Sa078408.
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Query Match
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EST.
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Stanford University
B55 California Ave, Palo Alto, CA 94304, USA
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Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.

1 (bases 1 to 365)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Walbot V
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             /lab_host="E coll XLOLR"

/note="Organ: juvenile vegetative shoots; Vector:
/note="Organ: juvenile vegetative shoots; Vector:
pAD-GAL4-2.1; Site_1: EcoRI; Site_2: XhoI; Equal amounts
of total RNA by weight from 4 tissue sources (see below)
were pooled, polyA+ RNA isolated, and cDNA synthesized for
EcoRI (5') and XhoI (3') directional cloning into lambda
Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
shoots 3 days after sowing/imbibing in wet soil. 2. Basal
1.5 cm shoots 6 days after sowing in wet soil from 6-8, and
the vegetative apex. 3. Non-green portions of developing
leaves 4-5 and the vegetative apex, including adult leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      949044 row: B
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                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Zea mays"
/cultivar="W64A"
/db_xref="taxon:4577"
/clone_lib="949 - Juver
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                                                                                                                                                                                                                                                                                                                                                         meristem"
primordia, 9
                                                                                                                                                                                                                                                                                                        /dev_stage="4 stages from 3-13 days after imbibing"
/lab_host="E. coli XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="immature leaf primordium and vegetative
                                                                                                                                                                                                                                                                                                                                                                                                           Moose"
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/tissue_type="leaf and stem, including leaf base"
/dev_stage="2 week old seedling (3 leaves)"
/lab_host="XL1-Blue"
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/db_xref="taxon:4577"
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Partially expanded
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AUTHORS

ACCESSION VERSION

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29; Conserv
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855 California Ave,
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Contact: Walbot V
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Fax: 650 725 8221
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//lab_host="E. coli XLOLR"
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Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
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1.5 cm shoots 6 days after sowing/imbibing in wet soil. 2. Basal
1.5 cm shoots 6 days after sowing - includes yellow
portions of developing leaves 1-5, primordia from 6-8, and
the vegetative apex. 3. Non-green portions of developing
leaves 4-5 and the vegetative apex, including adult leaf
primordia, 9 days after sowing. 4. Partially expanded and
greening leaves 4-5 at 13 days after sowing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     walbot@stanford.edu
949044 row: B col
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:4577"
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/cultivar="W64A"
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6.7e-05;
                                                                         DB 13;
6.8e-05;
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An EST database from Sorghum: pathogen-induced plants unpublished (2000) Contact: Cordonnier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 487)
                                                                                                                                                                                                                                                     mRNA sequence.
BE598350
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Department of Biological Sciences
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Plate: 614094 row: A column:
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                                                                                               Cordonnier-Pratt, M.-M., Gingle, A., Dean, R.,
                                                                                                                                                                                  Sorghum bicolor
                                                                                                                                                                                                     sorghum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stanford University
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/cultivar="W23"
/db_xref="taxon:4577"
/clone_11b="614 - root cDNA library from Walbot Lab"
/tissue_type="root"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: root; Vector: pBlueScriptII SK+; Site_1:
ECORI; Site_2: XhoI; 3-4 days old root tissue from Walbot
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/lab_host="XLOLR"
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library from Walbot Lab Zea mays cDNA,
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                                                                                                                           Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of P
Plant Sciences Building, Rm. 2502, Athens,
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
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Sequences have been trimmed
below Phred quality 16. The
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Tel: 706 542 1860
Fax: 706 583 0210
                                         Email: mmpratt@uga.edu
Seq primer: T7
                                                                                       Tel: 706 542 1860 Fax: 706 583 0210
                                                                                                                                                                                                                                          An EST database from Sorghum:
                                                                                                                                                                                                                                                                                   Cordonnier-Pratt, M.-M., Gingle, A., Paterson, A., Sudman, M. and Pratt
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                                                                                                                                                                                              Contact: Cordonnier-Pratt MM
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High quality sequence start: High quality sequence stop: 4
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/clone_lib="Pathogen induced 1 (PI1)"
/note="Organ: Anthracmose-infected leaves from
/note="Organ: Anthracmose-infected leaves from
/note="Organ: Anthracmose-infected leaves in its ite_1: XhoI;
two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRM421 of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after innoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from the pathogen."

1 94 c 125 g 136 t
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/db_xref="taxon:4558"
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                                                                                                                                Department of Plant Biology m. 2502, Athens, GA 30602-7271, USA
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(RHIZ2) Sorghum
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                                                                                                                                                                                                                                                                                                                      source
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                     112 AGCTTCTATATTAAGCTTCGATGAGAAGA 140
                                                                           Local
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Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW679158 535 bp mRNA linear EST 19-JUL-WS1_22_A09.g1_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
AW679158
                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences have been trimmed below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An EST database from Sorghum: water-stressed plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sorghum bicolor
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                                                           Conservative
                                                                                                                                  /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Water-stressed 1 (WS1)"
/clone_lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after /note="Organ: Mix of 5-week old plants on days 7 & 8 after water was withheld; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."

a 91 c 131 g 176 t
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/note="Organ: Rhizomes; Vector: pBluescript II from Lambda
Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made
Zap II, and the cloning vector lambda Zap II.
Clones to be sequenced were prepared by mass excision."
a 90 c 115 g 157 t
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/db_xref="taxon:132711"
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                                                    100.08; F1
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Pred. No.
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Pred. No.
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                                                         7.2e-05;
hes 0;
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7.1e-05;
                                                                                              DB 10;
                                                                                          Length 535;
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BG842699.2
EST.
sequence.
AW565695
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Tel: 515-294-0975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On May 25, 2001 this sequence Contact: Patrick S. Schnable Schnable Laboratory
                                  AW565695 568 bp mRNA linear EST 19-JUL-2000 LG1_348_A05.g1_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seg primer: primer T3 (ATT AAC CCT CAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qiu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEST39-A09.T3 ISUM4-TN Zea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 515-294-2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Iowa State University
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                                                                                                                                                                                                                      7.2%; ilarity 100.0%; Conservative
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/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST39-A09"
                                                                                                                                                                                                                                                                                                          resulting molecules were directionally cloned into the ECORI and NotI sites of the pT7T3PAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."
                                                                                                                                                                                                                                                                                                                                                                                                         as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were diested with NotI and size-selected. The resulting molecules were directionally cloned into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Seedling and silk"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="ISUM4-TN"
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, 7.2e-05;
thes 0;
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Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
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Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C.
An EST database from Sorghum: light-grown see
                              855 California Ave, Palo Alto,
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                 Department of Biological Stanford University
                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoldeae; Andropogoneae; Zea.
1 (bases 1 to 570)
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                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
AI978092
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614022D04.x2 614
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                                                                                                                                                       University
                                                                                                                                                                       Maize ESTs from various
                                                                                                                                                                                                                                                                                             Zea mays.
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706 583 0210
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ilarity 100.0%;
Conservative (
              walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Glone_lib="Light Grown 1 (LG1)"
/Glone_lib="Light Grown 1 (LG1)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: Xhol; Site_2: Ecol
: The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."

99 c 142 g 180 t
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/db_xref="taxon:4558"
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column:
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library from Walbot Lab
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04.
                                                                 CA 94304,
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7.3e-05;
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a; Poales; Poaceae; PACC
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330
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AW288508
                                                      29;
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Plate: 618068 row: C col
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                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Walbot V
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1 (bases 1 to 590)
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618068C02.x2
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                                                                                                                      /note="Organ: tassel; Vector: pAD-GAL4-2.1 (Hybrizap); Inbred tassel library from Schmidt lab" 138 c 112 g 157 t 1 others
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                                                                                                                                                                 /organism="Zea mays"
/cultivar="Ohlo43"
/db_xref="faxon:4577"
/db_xref="faxon:4577"
/clone_lib="618 - Inbred Tassel cDNA Library"
/tissue_type="tassel"
/dev_stage="tassel"
/dev_stage="tassel"
/lab_host="XLOLR"
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EcoRI; Site_2: XhoI; 3-4 days old root tissue from Walbot
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/cultivar="WZ3"
/db_xref="faxon:4577"
/clone_lib="614 - root cDNA library from Walbot Lab"
/tlssue_type="root"
/dev_stage="3-4 days old"
/lab_host="XLOLR"
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Inbred Tassel
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                                                   Score 29; DB
Pred. No. 7.3
0; Mismatches
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. 7.3e-05;
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cDNA Library Zea mays
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Zea mays
Center for Applied Genetic Technologies University of Georgia Riverbend Research Laboratory, Room 162, 110 Riverbend Road, Athens , GA 30602, USA Tel: 7065830162
                                                                                                   Unpublished, Paterson, A.H Unpublished (2002)
                                                                                                                                                                 Sorghum halepense
Sorghum halepense
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
Clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                   BQ656076
pRC0407 Sorghum halepense rhizome cDNA clone pRC0407, mRNA sequence. BQ656076
BQ656076
GG1:21788402
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Contact: Walbot V
Department of Biological Sciences
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Plate: 614022 row: D column:
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/db_xref="taxon:4577"
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/dev_stage="3-4 days old"
/lab_host="%LOLR"
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ECORI; Site_2: XhoI; 3-4 days old root tissue from Walbot
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b; Pred. No. 7.3
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library from Walbot Lab Zea mays cDNA,
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                                                                                                                                                                                                                                                                                                                           Email: mmprattega.edu
Sequences have been trimmed
below Phred quality 16. The
is 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,L.H.
An EST database from Sorghum:
Unpublished (2000)
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WS1_35_A09.g1_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA
                                                                                                                                                                                                                                                                High quality sequence start: High quality sequence stop:
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                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 706 542 1860
Fax: 706 583 0210
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                     156
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                   b
            /Clone_lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after
water was withheld; Vector: Lambda Zap; Site_1: XhoI;
Site_2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
110 c 148 g 198 t
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/tissue_type="rhizome"
/note="Vector: pBluescript SK(-); Site_1: EcoRT; Site_2:
/note="Vector: pBluescript SK(-); Site_1: EcoRT; Site_2:
XhoI; cDNA library was prepared from mRNA isolated from
the apical 2-3 cm of actively growing rhizomes of Johnson
grass (Sorghum halepense) and cloned into the EcoRI/XhoI
sites of lambda ZAP II (Stratagene)."
                                                                                                                                                             /organism="Sorghum bicolor"
/db_xref="taxon:4558"
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/db_xref="taxon:4560"
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Search completed: January
Job time : 2207 secs
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Matches 29; Conserv
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Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

(bases 1 to 613)
Walbot, V.
Walsot, S.

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A1691590.1 GI:4966734
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/dev_stage="ear length from 0.5 cm - 2.0 cm"
/lab_host="XLOLR (Stratagene)"
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/db_xref="taxon:4577"
/clone_lib="606 - Ear tissue cDNA library from Schmidt
lab"
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Pred. ŏ. is the number of results predicted by chance to have

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## ACCESSION VERSION KEYWORDS RESULT 1 AP003450 LOCUS DEFINITION Result No. SOURCE 000000 43. 42. 42. 40. 40. 40. 40. 40. 40. 40. 40. Score 39.8 39.2 38.2 38.2 37.8 37.8 37.8 37.4 37.4 0ryza sativa (japonica cultivar-group) genomic DNA, PAC clone:P0034C09. Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:P0034C09. Oryza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza. AP003450.3 Match 936 936 936687 9166679 9166679 919679 919679 9 1037 100625 544 173285 224297 1971 2529 2533 58198 111103 31522 100975 108992 142081 Length 158294 GI:16904687 DВ YSCSIT4C SCYDL47W SCCIVL37K AC095138 AC119153 AC119153 AC1191662 AL136162 AL13616276 SPBC26H8 AC087616 AC023950 AC130364 AC023950 AC130364 AC239501 AC130364 AC131768 AC121768 AC131768 AF003450 AY097414 AF275664 AY064136 AY064136 AY064283742 AF428374 AF305635 MDPPMD AF002050 AF003740 AF003740 AF004572 AF004572 E22116 ALIGNMENTS AY064136 Arabidops AY0847422 Arabidops AF428374 Arabidops AF428374 Arabidops AF305635 Pisum sat Z47076 M.domestica AP002050 Arabidops AC007980 Arabidops AC007980 Arabidops AC007980 Arabidops AC007980 Arabidops AC001724 Oryza sat AC091724 Oryza sat AC091724 Oryza sat AC091724 Oryza sat AC091728 S.cerevisia AC095138 Rattus no AC130153 Rattus no AC130153 Rattus no AC119135 Rattus no AC1136122 Homo sapi AC079014 Homo sapi AC079014 Homo sapi AC079015 Sequence AC087354 Homo sapi AC023950 Homo sapi AC023951 Sequence AC118963 Rattus no AC121768 Mus muscu AX29314 Sequence AX281620 Sequence AX281620 Sequence AX281620 Sequence AX37523 Sequence AX281620 Sequence AX375234 Homo sapi AC007129 Homo sapi AC007129 Homo sapi AC127462 Danio rer AC067792 Homo sapi AC130344 Homo sapi AL360334 Homo sapi AP003450 Oryza sat AY097414 Arabidops Description PLN 21-MAR-chromosome Arabidops 21-MAR-2002

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On Nov 12, 2001 this sequence version replaced gi:15887058.
Genes were predicted from the integrated results of the following: GENSCANI.0, BLASTNZ.0, BLASTNZ.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone ID.
A gene with identity or significant homology to a protein is classified based on the protein but with EST homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as a 'hypothetical' protein.

The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0034C09 clone has an overlap with p0519D04 (DDBJ: AP003455) at 5' end and with P043H09(DDBJ: AP003248) at 3' end.
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/db_xref="GI:18563401"
/translation="msklchHdgrvLlplllvaaaCldDpTgDTyDTaMCGAQASITC
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IDYASLTVSLADADVANGTCPVVSHNVTIPPAPSSLHLADTVGMLIFFERCAEGPAAN
APPKPSIHPLTCGENSEDAPTQSFLLPASPLPFGDLHRGCSAVYGVPVLGGSLPSD
ANDPAWRKDGYLTASLRKGFQMSWDRSDRCSRCELTSGKCGYNQNGKFLGCLCANGLUP
SDACKKISDSTLRAGVVGGGLSAVFALGLLTVFFVRKRKHKKVNSSSKLLKYSGSG
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VVAVKRLYNNSYRRVEQFVNEAAILSRLRHPNLVMFYGCTSSQSRELLLVYEFVANGT
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AU032946(S00005),C22642(S15001),D48660(S15001)
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/note="contains EST C26543(C12558)
unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:39947"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matsumoto, T. and Yamamoto, K. va nipponbare (GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .3354,3514. .3964,4062. .4343,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .3354,3514. .3964,4062.
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/gene="P0034C09.5"
join(23815. .23822.24395.
                                                                                                                                  'translation='mdegcildffgrogreprieggsaeffgrarberpirargr

Rerwigdlygdtahigmarevrrkgfgcamlrsgapggramarerydrahigr

Edggrorltglarrrganvaatraggrrkkgreprwtadgervihrskrhogflrgahigr

Edgrekerangsdsoegvrrwwnstaaaggerkgrsprodedsikgdwsisgvogthf

Rerwiglsgavevrrebasgggrowrkaburrgrepsertetelprkleftr

Sreegedeggtepegreprrodedptarkrallrragegeederpesrvtrepthulprosa

MDGDGASRAEATLARWRRERKRERLGDGAARRWGMSVLGGRKPTSWAVKEGRSRTWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(25181.
26825. .26964))
EKRPTAKRGAI"
                                                                    GGCGAERRRGRAAWAAAWRRLPGLTRRRPGSWPRVGERARDAGGGGVLPDFERRRRE
                                                                                                       QGVVTGGRGGMVPVGEKAKGEGGKGALPMPFREKGGRREDSASGSWTHAAWNGRARVA
                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="similar to Oryza sativa chromosome
p0031E09.21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(25181. .25819,25829. .26579,26587. .26790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TFSPSSTARRQTTHLNDAAVSEI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MRSGGRRDDGHAQMRAAGGARRQSSGGRARQRSGDGRQAERTAS
EEAGTMTSGVTEMRATMASASSSAGAAFPRQTGHEVWDESHMLMHSWWNTCPQAEICL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YSAHSDKCGKCERTKGWCGYRHNETSTTMDFTCFCDEGPTKSHCGTHASSPLTMSLLL FGVLLASDFRIGAVDIEFELLVERLKMINKPIRIINFSKQLLLH" join(23815...23822,24395...24764)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MPPPLLLLPVVLALFAAADASPSACRNATCGDVPVAYPFWLIDN SALGGGYPGLGELRCVUNTTLLLPFRTHDY RVLDIEYGKHTISTSVVKLTGGGAGPEHIGSS PHLHANLTIDDNSWLDLASSDSAITELY NCKSNSSLLSSTSVVKLTGGGAGPEHIGSS YVFLDGWITGEAYDYECETVVVAPVIDAHKKAMVDAHGGLPPADGSFGDVLSAGFELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="P0034C09.4"
complementing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MAHLPLLLLSFLLLIGVHASVSDGSPLPHTYNTSICSKSYKCGG
VITSYPSYLSHATGETYDYTOPSCGYTDLNITCSWDGSKQTPFLYDLNGDNYTILEINY
DSRTIVLUDTDALRGGSCPRYRHNITFSGADEWLDYTGPRDNLTFFFFGCHUCHVPLPWD
DSRTIVLUDTDALRGGSCPRYRHNITFSGADEWLDYTGPRDNLTFFFFGCHUCHVPLPWD
DSRTIVLUDTALRGGSCPRYRHNITFSGADEWLDYTGPRDNLTFFFFGCHUCHVPVNGSI
PGLTRFVDKNQINCKDFSNWPDGGDSFVFTSVELEAPMEYELASRCRQVIVVPVNGSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="contains ESTs AU100785(C50325),C26880(C50325)
unknown protein"
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/note="""
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complement/1000.3
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ITNVSLVDKEVVDDSSGCPRVDHNVTFAQGSWLFFPAGMSLDYLVFFLGCSFPNLFLP
PENIDPITCSFIGLIGPSYVLPKDQVPPGNWSQFCKTFEVPVVKYQQMDPKGDAWRKG
                                         IGKAAVHSAARGERERKQRESEERERKKRGDASLSLGVCSARAGRRRSGREERMGRAF
                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAB84593.1"
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/db_xref="GI:18565405"
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/db_xref="GI:18565404"
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/db_xref="GI:18565403"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(23815. .23822,24395.
/gene="P0034C09.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="hypothetical protein"
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26825

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DEFINITION ACCESSION
                                                                                                                      RESULT 2
AY097414
VERSION
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Best Local !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAAGGAGATGTCAAGGTCTTCACAGAGACCGAGGAAAAACAACCAGATTCCAGGGCCAAG 202
                                                                                                                                                                                                                                                AGTGTCATCACTCC
                                                                                                                                                                                                                                                                                AGGGGCATAACTTC
                                                                                                                                                                                                                                                                                                                                                                   TGCAATCTAATGCGTATGATTTTTCTGTTCTTTTAACCACATGTACAATAGACCATTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                TGCCATCTGATGCATTTCTGGTTTCTTTTGAACACAAGTACAAAAAAACCAACGGG 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAATCTGGAAGGGGTAAAGAACAATCAGATGGTGTTAATTGTGGAGGTTCAGATCATAA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAC-TGCTGTCCCATATTTCCTCTGACTTCATCAATTGTACAATTTTAGAAGTC-ATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAAAGAGAGGTCAAATTCTTCACAGAGACAGAGGAGAATAACCAGATGCGAGGACCGAG 79889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186;
                            AY097414 912 bp mRNA li
Arabidopsis thaliana AT3g19980/MZE19_3 mRNA,
AY097414
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/protein_id="BAB84596.1"
/db_xref="G1:18565409"
/tamslation="MLLSLCLRLLPLLLVLVAASHGDASGDTYDTSMCLQKPTTCGNV
SISYPFYFATKTKDINGSSNSYCGYPGLAIDCDDGKPILQLNGTEKYKVNYINYGSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(34381..35201,36446..37107,37314.

/gene="p003409.9"

join(34381..35201,36446..37107,37314.

/gene="p003409.9"
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/db_xref="GI:18565408"
/translation="MologskoTPFIOLNGENYTILEIIYDSRTIVLADTDALRGSCP
RVRHNVTFGQAYPWLQYTGSRDNLTFFFGCKLNLPPFIDPGLVSLADKHQINCKDFSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGSLERYAFRNNSEGEHSLTWEKLFDVVVGIARGLEYLHRGCNTRIVHFDIKPHNILL
DQEFCPKISDFGMAKLCSNKESIISIAGARGTIGYIAPEVYSKQFGAISSKSDVYSYG
MMILEMVGARERNIDANSESSSHYFPQWIYEHLDEYCINSSEIDVLYNCKYYLAVTKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NVSLADLEVVDDSGCPRVDHNVTIPQISWLFFSGISVDYLVEFLRCSFTTFAPKPAN
ENPIACGSFINLTR95FVFPDELVPFCMWSQLCEETFEVPVLKYQLMEMDSNGNAWNN
SGYAQVLRQGFINLTR95FVFPDESQCEESGGRGYSSAGEFICCLCPWGRVBSLFIN
LSDGRQVAVKMLKDSKGDGEEFINEVASISRTSHVNVVTLLGFCLHGSKRVLIYEYMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="contains ESTs C26880(C50325),AU100785(C50325)
unknown protein"
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QQPTLPRFGLDTATITRLPSFIYVTPQSGTAVQRHLTGACRGKNGANRFLRNRDLSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGFDLAWNSSKDEQCYKCEQSKGHCSYSQNRAFLGCLCSDGKYSTKDCRNNGASNSSA
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/gene="P0034C09.8"
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/gene="p0034C09.8"
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/gene="P0034C09.7"
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/codon_start=1
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73.2%;
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0: Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 113.2; DB 8;
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                                                                                         linear
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AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAS: Cheuk, R., Chen, H., Kim, C.J., Meyers, M.C., Shinn, P., Banh, J. Bowser, L., Chan, M.M., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Chan, M.M., Chang, E., Dale, J.M., Deng, J.M., Lin, J., Miranda, M., Jones, T., Karlin Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAs (RAFL CDNA: TRKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (15-APR-2002) Salk Institute Genomic Analysis Laboratory (SIGnAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis ORF clones
Unpublished
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Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G
Kawai,J., Lam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M.,
Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L., Sakurai,T.,
Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C.,
Yamamura Y V. C. Y., C. Shirosaki W Davids D u
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Cheuk,R., Chen,H., Kim,C.J., Meyers,M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                this work. Shinozaki, K. (RIKEN GSC) and contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                             VTVCGDIHGQFHDLMKLFQTGGHVPDTNYIFMGDFVDRGYNSLEVFTILLLLKARYPA
NITLLRGNHESRQLTQVYGFYDECQRKYGNANAWRYCTDVFDYLTLSAIIDGTVLCVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="This clone is
ecotype: Columbia"
                                                                                                                      EREVKFFTETEENNOMRGPRTGVPYFL"
                                                                                                                                                      TEFNHINKLDLVCRAHQLVQEGLKYMFQDKGLVTVWSAPNYCYRCGNVASILSFNDNM
                                                                                                                                                                                   GGLSPDVRTIDQIRLIERNCEIPHEGPFCDLMWSDPEDIETWAVSPRGAGWLFGSRVT
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/db_xref="G1:20453383"
/translation="MDLDQWISKVKDGQHLSEDELQLLCEYVKEILIEESNVQPVNSP
                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
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24.1%;
Score
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96.8;
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DВ
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Length 912;
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Narusaka, M.,
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PLN 05-DEC-2001

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Toriumi, M.,

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REFERENCE
AUTHORS
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TITLE
                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                          Matches 164;
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                                                      789 GCCGCGCGCACCAACTTGTACAAGAAGGTCTTAAGTACATGTTCCAAGATAA-AGGCCTT 847
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65 GAACTTGTGTGGTCTGCACCCTAATTATTGCTCAGATGTGGCAATGGAGCTTCTATATTA 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1068)
Kang, J.G., Kim, D.-H. and Park, C.-M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (05-JUN-2000) Kumho Life & Environmental Science Laboratory, 1 Oryong-Dong, Puk-Gu, Kwangju 500-712, Korea
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Unpublished
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Isolation of cDNA clone encoding a putative
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                                                                                                                                                                                                                                                                                                                                                               /product="serine/threonine protein phosphatase"
/protein_id="AAK69404.1"
/protein_id="AAK69404.1"
/db_xref="Gi:14485206"
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/translation="MDLDQWISKVKDGOHLSEDLECYTVGYVGYVGYTGHILLLKARYPA
NITLLRGNHESRQLTQYYGFYDECQRKYGNAMARYCTDVFDYITLSAIIDGTVLCYH
GGLSPDYRTIOQIRLERNCEIPHEGPFCDLMWSDPEDIETMAVSPRGAMLFGSRVT
TEFNHINKLDLVCRAHQLVQEGLKYMFQDKGLVTVWSAPNYCYRCGNVASILSFNDNM
                                                                                                                                                                                                                                                                                                              EREVKFFTETEENNOMRGPRTGVPYFL 205 c 253 g 311 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="STPP"
98. .1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="STPP"
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/db_xref="taxon:3702"
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73.28;
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in phosphatase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C.,
Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C.,
Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M.,
Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A.,
Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M.,
Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L.,
Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M.,
Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K.,
Davis, R.W., Theologis, A. and Ecker, J.R.
Diffect Submission
Diffect Submission
Submitted (27-NOV-2001) Salk Institute Genomic Analysis Laboratory
(SIGnAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGATTCCAGGGCCAAGGGCTTGGAATCCCATATTTCCTTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt AGTTTCAATGACAACATGGAAAGG-GAAGTGAAGTTCTTCACAGAGACAGAAGAAGAACAA}
                                                                                                                                                                                                                                                                         The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Shinn,P., Chen,H., Cheuk,R., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J. Bowser,L., Chang,E., Dale,J.M., Goldsmith,A.D., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K., Yamamura, Y., Yu,G., Yu,S., Davis,R.W., Theologis,A., and Ecker,J.R.
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Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Goldsmith, A.D., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nauyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Tooriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
                                                                                                                                       Shinn,P. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSF contributed equally to this work as PIs.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        collection and clustering of RAFL cDNAs (RAFL cDNA: 'Ri
Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis cDNA clones Unpublished
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                    /organism="Arabidopsis
/db_xref="taxon:3702"
/chromosome="3"
                                                                                   thaliana"
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Ş 밁 Qy

uted equally (SSP/Salk)

RIKEN Ishida,J.,

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JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                            JOURNAL REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164;
Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA Malibu, CA 90265, USA This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Spermatophyta; Magnollophyta; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 1312)
Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P.,
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Arabidopsis thaliana clone 35230 mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AY087422
AY087422.1
                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                    Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R.
                                                                                                                                                                                                                                                                             Full-Length cDNA from Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                        Genome Biol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                  annotation
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/db_xref="G1:17381249"
/db_xref="G1:17381249"
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VTVCGD1HGQFHDLMKLLQTTGGHVPDTNYIFMGDFVDRGYNSLEVFTILLLLKRRYPA
NITLLRCNHESRQLTQVYGFYDECQRKYGNANAWRYCTDVFDYLTLSAIIDGTVLCVH
GGLSPDVRTIDQIRLIERNCEIPHEGPFCDLMWSDPEDLETWAVSPRGAGWLFGSRVT
TEFNHINKLDLYCRAHGLVQEGLKYMFQDKGLVTVWSAPNYCYRCGNVASILSFNDNM
EREVKFFTETEENNQMRGPRTGVPYFL"
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GTCGCGCTCACCAGCTTGTACAAGAAGGTCTCAAGTACATGTTCCAAGATAA-AGGTCTT 928
                                                                                                                                                                                                                                                                                                                                                       GCCGGGCTCACCAGCTGGCCCAGTGAAGGCTTAAAGACATGTGCCAGGAGAAGGGGCCCTT 64
                                                              AGCTTCGATGAGAAGAAGGAAAGGAGATGTCAAGGTCTTCACAGAGACCGAGGAAAACAA 184
                                                                                                                                        GTAACTGTGTGGTCTGCGCCTAATTACTGCTACCGTTGTGGGAATGTGGCTTCTATATTG 988
                                                                                                                                                                                                              GAACTTGTGGTCTGCACCCTAATTATTGCTCAGATGTGGCAATGGAGCTTCTATATTA 124
AGTTTCAATGACAACATGGAAAGG-GAAGTGAAGTTCTTCACGGAGACAGAAGAAGAACAA 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATC). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or LAer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NITLLRGNHESRQLTQVYGFYDECQRKYGNANAWRYCTDVFDYLTLSAIIDGTVLCVH
GGLSPDVRTIDQIRLIERNCEIPHEGPFCDLMWSDPEDIETWAVSPRGAGWLFGSRVT
TEFNHINNLDLVCRAHQLVQEGLKYMFQDKGLVTVWSAPNYCYRCGNVASILSFNDNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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/protein_id="AaM64970.1"
/protein_id="AaM64970.1"
/db_xref="GI:21593021"
/translation="MDLDQWISKVKDGQHLSEDELQLLCEYVKEILIEESNVQPVNSP
/TYCGDIHGQPHDLMKLFQTGGHVPENYIFMCDFVDRGYNSLEVFTILLLKARHPA
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/db_xref="taxon:3702"
/clone="35230"
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70.4%;
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1 (bases 1 to 1366)
Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J.,
Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y.,
Bowser, L., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G.,
Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G.,
Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M.,
Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K.,
Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C.,
Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K.,
Davis, R.W., Theologis, A. and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana At1g50370/F1413_10 mRNA, complete cds.
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                                                                        Arabidopsis cDNA clones
to 1366)
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1099 237

PLN 02-MAY-2002

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BASE CO
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Matches 164
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                           TCAAATGAGAGGGCCAAGGAC-AGGTGTTCCTTATTTCCTGTGATTCATGATG 1082
                                                   CCAGATTCCAGGGCCAAGGGCTTGGAATCCCATATTTTCCTTTGACTTCAGGTG
                                                                                                                GTAACTGTGTGGTCTGCGCCTAATTACTGCTACCGTTGTGGGAATGTGGCTTCTATATTG
                                                                                                                                                                                                                                                            GAACTTGTGTGGTCTGCACCCTAATTATTGCTCAGATGTGGCAATGGAGCTTCTATATTA 124
                                                                                                                                                                                                                                                                                                                                                          GCCGGGCTCACCAGCTGGCCCAGTGAAGGCTTAAAGACATGTGCCAGGAGAAGGGGCCCTT 64
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164; Conserv
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RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, 1 Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J.T., Liu, S.X., Miranda, M., Naguen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, B.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C. Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAs: Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Shinn, P., Banh, J. Bowser, L., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (05-OCT-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037
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TEFNHINNLDLVCRAHQLVQEGLKYMFQDKGLVTVWSAPNYCYRCGNVASILSFNDNM
EREVKFFTETEENNQMRGPRTGVPYFL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MDLDQWISKVKDGQHLSEDELQLLCEYVKEILIEESNVQPVNSP
VTVCGDIHGQFHDLMKLFQTGGHVPETNYIFMGDFVDRGYNSLEVFTILLLLKARHPA
NITLLRGNHESRQLTQVYGFYDECQRKYGNANAWRYCTDVFDYLTLSAIIDGTVLCVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="At1950370/F1413_10"
/protéin_id="AAL16304.1"
/db_xref="GI:16226940"
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/note="ecotype: Columbia"
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                                                                                                                                                                                                                                         TCAGATGAGAGGGCCAAGGACAGGTGTTCC
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                                                                                                                                                                                                                                                                                                                                                                                AGCTTCGATGAGAAGGAAAGGAGATGTCAAGGTCTTCACAGAGACCGAGGAAAACAA 184
                                                                                                                                                                                                                                                                                                                                    AGTTTCAATGAAAATATGGAGA-GAGAAGTTAAGTTTTCACTGAAACAGAGGAGAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146;
                                              (PPX).
Z47076
                                                                                             M.domestica Borkh mRNA
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serine/threonine protein
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                                                                                                                     MDPPMD1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
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/protein_id="AAM21172.1"
/protein_id="AAM21172.1"
/db_xref="GI:20385063"
/translation="MDLDQWISKVKDGQHLLEDELQLLCEYVKEILIEESNVQPVNSP
/translation="MDLDQWISKVKDGQHLLEDELQLLCEYVKEILIEESNVQPVNSP
/translation="MDLDQWISKVKDGQHLLEDELQLLCEYVKEILIEESNVQPVNSP
/translation="MDLDQWISKVKDGQHLLEDELQLLCEYVKEILIEESNVTFILLLLKARYPA
NITLLRGNHESRQLTQVYGFYDEQRKYGNANAWRYCTDRVDYLTLSANIDGTVLCVH
GGLSPDIRTIDQIRVIENNCEIPHEGPFCDLMWSDPEDLETWAYSPRGAGWLFGSRVT
SEFNHINNLDLLCRAHQLVQEGLKYMFTDKGLVTVWSAPNYCYRCGNVASILSFNENM
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/db_xref="taxon:3888"
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Pred. No. 1.7e-14;
0; Mismatches 62;
                                                                                             for serine/threonine protein phosphatase
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                                                                                                                                                                                                                                                                                                                                        CCAGATTCCAGGGCCAAGGGCTTGGAATCCCATATTTCCTTTGA 228
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                                                                                                                                                                                                                                                                                                    CCAGATGAGAGCACCGAGGAC-AGGAGTACCTTATTTCTTATGA 959
                                                                                                                                                                                                                                                                                                                                                                             AGTTTTAATGACAATATGGAGA-GAGAGGTGAAGTTCTTCACTGAAACAGAGGAGAACAA 916
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                                                                                                                                       31522 bp
Arabidopsis thaliana genomic DNA,
AP002050 BA000014
AP002050.1 GI:8051658
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               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                      Arabidopsis thaliana
                                                                                            clone:MZE19
                                                                                                              Arabidopsis thaliana (strain:Columbia) DNA,
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Agronomiques, Avenue Marechal Juin, 13,
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Expression of PPX and PP2A phosphatase m
Plant Sci. (1995) In press
2 (bases 1 to 1324)
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SEFNHINNLDLVCRAHQLVQEGLKYMFQDKGLVTVWSAPNYCYRCGNVASILSFNDNM
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/translation="mildowiskykegohiledelqilceyvkeilieesnvqpvnsp
/translation="mildowiskykegohiledelqilceyvkeilieesnvqpvnsp
vtvccdihqophilmkilgojoghvpeinyiewgdfvdrgynslevftilleaiidgtvlcvh
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/protein_id="CAA87385.1"
/db_xref="GI:1143511"
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/db_xref="taxon:3750"
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Pred. No. 3
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Address for correspondence: Roos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MZE19
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
MetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is MPN9 and the 3' clone is MAL21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S. Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
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                                                                                                                                         GGGSGIEYEILKTNPILEAFGNAKTLRNDNSSERGKLIEIHFSESGKISGAQIQTFILI
EKSRVVQCABGERSYHIFYQLCAGASPALREKLNLTSAHEYKYLGQSNCYSINGVDDA
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QSPGYVEQGLYKAGGADSQRLSVATKFKSQLFTLMYRLGFTLYENLADRDPL
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join(1527. .1865,2003. .2104,2187. .2330,2455. .2605,

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4013. .4116,4218. .4356,4652. .4770,5097. .5249,5447. .5536,

5673. .5750,5911. .6069,6192. .6398,6627. .6832,6920. .7055,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDILDGVDDLMQLSYLNEPSVLYNLNYRYNQDMIYTKAGPVLVAVNPFKEVPLYGNRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis
/strain="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="MZE19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:3702"
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SDCELVEHLDCSEVSLINAKEKGIFDGDEEWRKKINALVPENGVVKHIKTGENIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MGSLSGIIQRPLVAAAAVITASVSADVSERFSSLRSLVRGSESE
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SRMGAIYSLIVREEEILMEERRRAFGSGFEVRKERDEDIDLVVPPVFSFCTKVLDAKE
QIEAREMYWEVVSSDTSKEGYLERAEERLLGCIEKNPFVGEPHVLLSQVYLGKKRFKE
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                                                                                                                                                                                  join(23092..23197,23303..2
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                                                                                                                                                                                                                                                           DFMYNYFSRDVTASVGYDYMLRQARVRGKIDSNGVASALLEERLSMGLNFLLSAELDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(19425. 19551,20049. 20167,20213. 20317,20601. 2
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TEFNHINKLDLVCRAHQLVQEGLKYMEQDKGLVTVWSAPNYCYRCGNVASILSFNDNM
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15977 ..16048,16418 ..16501)
/note="gb|AAD50050.1
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join(13748. .13828,14115. .14261,14349. .144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEREAEKGLLLLLQWGSPWDKRMSWEGWIAWVRVLLMKSQDQSWPDVSWGILNLGLVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein"
                                                                                                                                                                                                          .23979,24508. .24579,24654. .2
1,26566. .26787,26911. .27474,
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QAVLRAIMLRRTKGTLLDGKPIINLPREVVNILSQVDFSYKKLEADSRSQFKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESSCKQETEALVLDADDESDNAKHESGSHVKPELKVSSNSETSVLSACGNDENDSSDM
EKAEDEBANGSTRAFQWKRPAAGTLI VCPAWARELDEKVSEESKLSVLVYHGS
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VVVGASKKSKRRGRKSTNDTSSEPDCGPLGKVGWFRIVLDEAQTIKNYRTQMARSCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGTNNIRNAGGSRFGADYSHPAVSAVGNKSTFGDHYSGAHAEIGIQRGVNGVRILPPS
LTHGTSASVLHHAGSSDPMHRFGGGEDRNPDNDERLVYQAALQVLNQPMTESDLPPGT
                                                                                             WNPTTEDQAIDRAHRIGQTRPVTVTRITIKDTVEDRILKLQEEKRTMVASAFGEEHGG
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Query Match
Best Local (
16477 GAC-TGGAGTTCCGTATTTCCTATGA 16501
                                                                                                                                 143 GAAAGGAGATGTCAAGGTCTTCACAGAGACCGAGGAAAACCAGATTCCAGGGCCAAG 202
                                                                                    GGAAAGGGAAGTGAAGTTCTTCACAGAGACAGAAGAGAACAATCAAATGAGAGGGCCAAG 16476
                                       GGCTTGGAATCCCATATTTCCTTTGA 228
                                                                                                                                                                                                Similarity
                                                                                                                                                                              Conservative
                                                                                                                                                                                                10.8%;
                                                                                                                                                                           Score 43.6; DB 8; Length 31522;
Pred. No. 0.092;
0; Mismatches 19; Indels 1;
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Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Nguen, M., Brooks, S., Buehler, E., Chao, Q., Dunn, P., Gonzalez, A., Khan, S., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Direct Submission
Submitted (07-JUL-1999) DNA Sequencing and Technology Center, Submitted (07-JUL-1999) Each Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 943 2 (bases 1 to 100975)

2 (bases 1 to 100975)

Federspiel, N. A., Palm, C. J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P. Gonzalez, A., Kremenetskala, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskala, V., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskala, V., 1 (bases 1 to 100975)
Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P. Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vysotskaia, V.S., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Submitted (17-AUG-1999) DNA Sequencing and Technology (Stanford University, 855 California Avenue, Palo Alto, Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. Direct Submission Yu,G., Walker,M., Unpublished Arabidopsis thaliana AC007980.1 GI:5391457 Arabidopsis thaliana Arabidopsis thaliana. (bases 1 to 100975) Ecker, J., Theologis, A. a sequence. Yu,G., Ecker,J., 100975 bp chromosome Theologis, A. and Davis, R.W. and Davis, R.W. I BAC F14I3 linear genomic sequence, PLN 28-FEB-2001 CA 94304, Dunn, P., Dunn, P.,

CA 94304,

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
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Genes with similarity to proteins in the databases are described as
'putative', '-like' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'. The
software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge,
http://gnomic.stanford.edu/
chris/GENSCANW.html), Fexa (V.Solovyev & A.Salamov, Sanger Centre,
http://genomic.sanger.ac.uk/), and NetPlantGene (S.M. Hebsgaard, et
al., CBS, Technical University of
Denmark,http://www.cbs.dtu.dk/NetPlantGene.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (28-FEB-2001) DNA Sequencing and Technology (
Stanford University, 855 California Avenue, Paio Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A.
and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLEPHETLSGSSGANGHTKTGLINLDSRNGFESKPLPRAEHTHLPGNGSIVTSRIPN
ISVGDYEKFSKOOAFKRTHPPTTSRPPPPPPPDIGTSNGNASHTRDLS
ISVGDYEKFSKOOAFKRTHPPTTSRPPPPPPPDIGTSNGNASHFRGGAHDDLGMGRVT
NGTRILPSVAHGTSASPSHFNGLSDPMHRNGIGERNSENDERLIYQAALQTMCNEA
LLFFLEDKREGIGTFTIVAFVSYFALLHOGXDPHLKSLYFHLNSPGTESTOVRGRETC
WSSFGSPYEASGIQVYIIFQYLSEWSCULNTVVSQKIALAMMFQKETNSLHCMGGILA
DDQGLCKTVSTIALILKOMHEAKLKSKNSGNQEAEALDLDADDESNAFEKPESKASN
GSGVNCDSGIKKAKGERSTSTRKFNKRRPAAGTLIVCPASVVRQMARELDEKVTDEA
KLSVLIIYHGGNRTKDPIELAKYDVMTTYAIVSMEVPKOPLVDDDENDEKNSEKYGLA
SGFSINKKRKNVGTTKKSKKKGNNNAGDSSDDDSGTLAKVGWFRVVLDBAQTIKNH
RTQVARACCGLRAKRRPCLSGTPIQNTIDDLYSYFREKKDPYAVYKSFCHQIKCGIS
RNSLOGYKKLQAVLRAIMLRRTKGTLLDGOPINLPKTINLSQVDFSVEERSFYVKL
ESDSRSGFKAYAAAGTLMQNYANILLMLLRLRQACDHPOLVKRYNSDSVGRVSEEAVK
KLEKEDLYSLLSRLESSPICCYCHDPPEDPVYTLCGHIFCYQCYSDYITGDEDTCPAP
RCREQLAHDVVFSKSTLRSCVADDLGCSSSEDNSHDKSVFQNGEFSSKIKAVLDILQ
SLSNQGTSNSTONGQMASSSQQPNDDDDDDDDVTIVEKTSLKSTPSNGGFIKTIIFS
OWTGMLDLVELSLIENEETRALDETRANSLIERTRKDLAVKEF*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(6533. .8700)
/gene="F14I3.2"
complement(join(6533. .6586,6685. .6780,6872. .6955,
complement(join(6533. .6586,6685. .6780,6872. .6955,
7036. .7104,7261. .7362,7550. .7615,7697. .7747,8020.
8208. .8289,8574. .8700))
/gene="F14I3.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(<1. .4027)
/gene="F1413.1"
complement(join(<1. .567,690. .908,1119. .1249,1596. .2526,
complement(<1. .567,690. .908,1119. .1249,1596. .2526,
complement(<1. .567,690. .908,1119. .1249,1596. .2526,
complement(<1. .567,690. .908,1119. .1249,1596. .2526,
complement(join(<1. .567,690. .908,1119. .1249,1596. .1249,
complement(join(<1. .567,690. .908,1119. .1249,1119. .1249,
complement(join(<1. .567,690. .908,1119. .1249,1119. .1249,
complement(join(<1. .567,690. .1249,11
                                                  LKPELFEGFRLDYNKSLNQKFFLSHSLCIDASNSILMGPTEVPNPTPSSEIIKIPTAN
YDFGAGFIDPKLTDEEDKSQGHLVIDYKGSDYRTQLQLGNNSYYAANYIQHVTPHLSL
GGEAFWLGQQLMSGVGYAARYETDKTVASGQIASTGVAVMNYVHKVSEKLSFATDFIY
                                                                                                                                                                             /protein_id="AAD50049.2"
/protein_id="AAD50049.2"
/db_xref="GI:33162531"
/db_xref="GI:33162531"
/translation="MEGFSPPINTAQVDAKTKLDEKVDYSNLPCPVLYEELNREATMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                portion of the gene"
NYLSRDVTASVGYDLITRQSRLRGKVDSNGVVAAYLEEQLPIGLRFLLSAEVDHVKKD
                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Hypothetical protein"
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/db_xref="GI:5734771"
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/clone="F14I3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 to 100975)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .100975
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, CA 94304,
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VBVRF01, gb|Z3
greater than 6
phosphatases"
                                                                                                                                                                                                                                                                         complement()oin(19749...20405,20494...20561,20665...20811,20897...21026,21113...21248,21375...21580,21772...21978,21215...21233,22491...22568,22683...22772,22907...23059,23230...23348,23550...23688,23778...23881,24055...24132,24346...24409,24517...24682,244985...25235,25382...25255,25614...25715,25853...26167))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLRVLTPRVDGIDSSVSHRGNHFFIQRRSTEFYNSELIACPVDDTSKTTVLLPHRESV
KIQEIQLFRDHLAVFERENGLQKITVHRLPAEGQPLEGLQGGRNVSFVDPVYSVDSTE
SEFSSRYLFRKYCSMKTPPSVYDYDMDSTSVYKKIDFVLGGFDASNYVTERKWVAAS
DGTQIPMSIVYNKKLAKLDGSDPLLLYGSGSFSEFSFFKASRLSLLDRGFTFVIAN
VRGGGEMGRQWYENGKLLKKKNTFTDFIACAERLIELKYCSKEKLCMEGRSAGGLLMG
AVVNMRPDLFKVVIAGVPFVDVLTTMLDPTIPLTTSEWEEWGDPRKEEFYFYMKSYSP
VDNVTAQNYPMMLVTAGLNDBRWMYSEPGKWVAKLREMKTDNNVLLFKCELGAGHFSK
/translation="MAHKVKASFQSLKTMPADYRFLGSPISDHLETNLITPPNGHLKN
GVNGTASSVGGMDSVNEDSPYSVRSILMGERSSIGDGDSILPLEDSNDRKWSDTRVYA
RKKYLOFWYQLDHQRWELGKIMSTGGEESVILVTEGKYULKYKSETUPAHDDILDSVD
DLMQLSYLNEPAVLYNLEYRYNQDMIYTKAGPVLVAVNPFKEVPLYGNRNIEAYRKRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTVCGDIHGQFHDLMKLFQTGGHVPETNYIFMGDFVDRGYNSLEVFTILLLLKARHPA
NITLLRGNHESRQLTQVYGFYDECQRKYGNANAWRYCTDVFDYLTLSAIIDGTVLCVH
GGLSPDVRTIDQIRLIERNCEIPHEGPFCDLMWSDPEDIETWAVSPRGAGWLFGSRVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(15183...15266,15621...15692,15782...1587)
15975...16118,16224...16274,16387...16497,16857...16914,
17131...17198,17284...17430,17881...17961))
//gene="F1413.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HCRRLITDNKAEPSVYDTMPTGPDAPPEHVILDENTKAQEHDYYRIGAFKASPDHKLV
AYAEDTKGDEIYTVNVIDSEALKPVGQQLKGLTSYLEWAGNDALLYITMDEILRPDKV
WLHKLGTEQSSDVCLYHEKDDMFSLELHASESHKYLFVASESKTTRFVFSLDVSKTQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(10670. .10748,10841. .10964,11094. .11142,
11234. .11299,11516. .11881,11975. .12133,12413. .12704,
12911. .13257,13477. .13671,13773. .14056,14204. .14375))
/gene="F1413.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MKATEEAKEAGALLSYDPNLREPLWPSPEEARTQIMSIWDKADI
IKLLLYTLGEKGCRYYTKDFHGSVETFHVDAVDTTGAGDSFVGALLNQIVDDQSVLEE
EERLRKVLRIANACGAITTTKKGAIPALPTDCEALSFLKRQVEQ"
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/gene="F1413.3"
/oin/9178 .9315,9403. .9450,9539.
/gene="F1413.3"
                                                                                                                                          /codon_start=1
/protein_id="AAD50052.1"
/db_xref="GI:5734787"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(19749. .26167)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEFNHINNLDLVCRAHQLVQEGLKYMFQDKGLVTVWSAPNYCYRCGNVASILSFNDNM
EREVKFFTETEENNQMRGPRTGYPYFL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAD50050.1"
/db_xref="GI:5734785"
/translation="MDLDQWISKVKDGQHLSEDELQLLCEYVKEILIEESNVQPVNSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(15183. .17961)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGRFEKLQEDAFTFAFMMKVLDMIPASG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(10670 .14375)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Similar to fructokinase; Similar to frutokinase,
but smaller and lacking some of the sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="phosphoprotein phosphatase; Location of ESTs
VBVRF01, gb|Z33786 and ATTs2101, gb|Z29155. Protein has
greater than 65 % identity with mammalian protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LREENHYTDFVMSGTKQFENQLFAEIRGRIKEDDISAPLRKGPYYYYEKNLQGKEYIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAD50051.1"
/db_xref="GI:5734786"
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/db_xref="GI:5734772"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="F14I3.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="F1413.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="F14I3.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            frutokinase"
                                                                                                                                                                                                                                               note="Highly similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MAESRSPPVAKKVEHVMEMFGDVRVDNYYWLRDDSRTNPDMLSY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Similar to oligopeptidases"
                                                                                                                                                                                                                                                  myosin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .9655,9732.
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAAGCTTCGATGAGAAGGAAGGAAAGG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGTAAAGGTGTGGTCTGCGCCTAATTACTGCTACCGTTGTGGGAATGTGGCTTCTATAT 15641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGAACTTGTGTGGTCTGCACCCTAATTATTGCTCAGATGTGGCAATGGAGCTTCTATAT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (E-mail:tsasaki@nias.affrc.go.jp, Url:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
On May 24, 2002 this sequence version replaced gi:14422458.
Genes were predicted from the integrated results of the following: GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Only in Database (2001)
2 (bases 1 to 108992)
Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              סמאבענט DNA linear PLN 03-AUG-2002 Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 7, BAC clone: סידור BAC cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (13-JUN-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
                                                                                                                                                                                                                                                                                           (http://www.softberry.com/), GeneMark.hmm (http://opal.biology.gatech.edu/GeneMark/), GlimmerM (http://opal.biology.gatech.edu/GeneMark/), GlimmerM (http://opal.org/tdb/glimmerm/glmr_form.html), RiceHMM (http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor (http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor (http://bloinformatics.iastate.edu/cgi-bin/sp.cgi), BLASTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nipponbare(GA3) genomic DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone:0J1118
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                                                         NCBI NonRedundant Protein database with BLASTP.
                                                                                                                   (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against
                                                                                                                                                                                                                                                    Protein database, nr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AP003740.2 GI:21202839
dentified cDNA sequences using BLASTN with the corresponding DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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QCTEGERSYHIFYQLCAGASPTLREKLMITSAKQYNUZKGSNCYSINGYUDAERPHAV
KEALDIYHVSKEDQENYFAMLAAVLMLGNVSFTIIDNRNHYEPEPDESISTVAKLIGC
KEALDIYHVSKEDQENYFAMLAAVLMLGNVSFTIIDNRNHYEPEPDESISTVAKLIGC
NINELKAALSKRMKVNNDTIVQKLTLSQAIDARDALAKSIYACLFDWLVEQINKSLA
VGKRRTGRSISILDIYGFESFNKNSFEQFCINYANERLQQHFNRHFKLEQENYIQDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIRGELVRRCAGDIGWLSSGGTKRNESDEVLVKASYLSDLQRRVLRTEAALREKEEEN
DILRQRVQQYDNRWSEYETKMKSMEEIWQKQMKSLQSSLSIAKKSLEVEDSARNSDAS
VNASDATDLDSGGSHYQMGHGRSRSVGVGLSVISRLAEEFGQRAQVFGDDRKFLMEVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQGLVLQQLRCCGVLEVVRISRSGFPTRMFHHKFARRYGFLLLENIAAKDPLSVSVAI
LHQFNILPEMYQVGYTKLFFRTGQIGVLEDTRNRTLHGILRLQSYFRGHQARCRLKEL
KTGITILQSFVRGEKMRKEYTELLQRHRASAAIQSHVKRRIASQQYKATVDASAVIQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDRGKAFTVAHYAGEVTYETTGFLEKNRDLLHSDSIQLLSSCSCHLPQAFASSMLIYS
EKPLVGPLHKAGGADSQRLSVATKFKGQLFQLMQRLGNTTPHFIRCIKPNNVQSAGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGQVEANLNPDRELRRLKQMFETWKKDYGGRLRETKLILSKLGSEETGGSAEKVKMNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {	t IDWTRVDFEDNQECLSLFEKKPLGLLSLLDEESTFPNGTDLTLANKLKQHLNDNSCFR}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 100975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                   ESTs represent the
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SOURCE

ORGANISM

KEYWORDS

/ERSION ACCESSION DEFINITION

AP003740/c RESULT 11 밁 Š 밁

15640 123 Matches

63

JOURNAL REFERENCE AUTHORS TITLE

JOURNAI

REFERENCE

AUTHORS TITLE

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence. The orientation of the sequence is from -21M13 to M13rev of the BAC clone. This sequence of OJ1118_B03 clone has an overlap with P0592C06 (DDBJ:AP00157) clone at the 5' end and with P0686C05 (DDBJ:AP004572) at the 3' end. The sequence was generated by combining Monsanto and RGP-Japan sequencing data. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                    TIPTIGENVETVEYKNISFTVWDVGGQDKIRPLWRHYFQNTQGLIFVVDSNDRDRVVE
ARDELHRMLNEDELRDAVLLVFANKQDLPNAMNAAEITDKLGLHSLRQRHWYIQSTCA
TTGEGLYEGLDWLSSNIASKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13632. .13713,13847. .13852)
/gene_"OJI118_B03.3"
/join(11450. .11597,12715. .12785,12991. .13110,1329
13632. .13713,13847. .13852)
/gene_"OJI118_B03.3"
/note="contains ESTs D40795(S2947),AU081605(S2947)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(10633. .10839)
/note="5' LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAC06913.1"
/db_xref="G1:22093617"
/db_xref="G1:22093617"
/translation="mrarrmivvtagstelvsaagstieaerrsllcaggvwegmra
GEAESSTRQREATAASTPIPVACGSAGGVPCVPAAGDADAVSSASIRAAAVNGECRRSI
EDPSAGFSRANRRWKADGTILRPSVKGDDGGTSMRIWADSFGIGDHVSQRLV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(3946..8619)

/gene="0J1118_B03.1"

/note="probably inactive due to frameshift(s) in probably inactive due to stop codon(s) in CDS pseudogene, copia polyprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="0J1118_B03.1"
                                                                                         /note="hypothetical protein
predicted by GeneMark.hmm e'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similar to Oryza sativa chromosome1,BAA90382"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(3276. .3488)
/note="3' LTR"
/protein_id="BAC06915.1"
/db_xref="GI:22093619"
                                                                                                                                                                                                                                                                                                                                                                                                                            /product="ADP-ribosylation factor
/protein_id="BAC06914.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="0J1118_B03.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene-"0J1118_B03.2"
join(9485. .9573,9643. .9940,10027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(9485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:39947"
/chromosome="7"
                                                                                                                                                    jōin(15518. .]5613,15722. .15796)
/gene="0J1118_B03.4"
                                                                                                                                                                                                         /gene="0J1118_B03.4"
                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="GI:22093618"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(11450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="0J1118_B03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa
                                                             /codon_start=
                                                                                                                                                                                                                                                                                                                                                                 translation="MGLAFGKLFSRLFAKKEMRILMVGLDAAGKTTILYKLKLGEIVT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTR"
                                                                                                                                                                                                                                           .15613,15722. .15796)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .11597,12715.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .12785,12991. .13110,13298. .13416,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .10092,10185.
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CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                             /translation="MRSCCCCCPCPAALGIGIGPPLRSFLDYDALQSLALALIYLQI
GCALIGSLGALENGVLYINLVIGLEAVVAIESSSQTLGRTYAVLLFFAIVLDYAWFIL
FSHAINITPERKYGQLFVLSLKLALAMQIIGFMYRLGVSSTPYHEWYDGRNSFL
FSHSSSYRRNSMADDILGGSIYDPAYYSSLFADVRNNTCTHQGDKQSGNDSGSTSAG
GSPRLKSFASRSFVANDLEDHTFQFSDFS"
Join (36427. 36609, 38877. 38975, 39825. 39950,40746. .4082
40868. .41155,41199. .41801)
Join (36427. 3609),38877. 38975,39825. .39950,40746. .4082
40868. .41155,41199. .41801)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(16653..16790,16994.
/gene="OJ1118_B03.5"
complement(join(16653..16790,16994.
/gene="OJ1118_B03.5"
                           /note="hypothetical protein predicted by FGENESH etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32801. .32899,33193. .33231)
/gene="OJI118_B03.9"
join(29910. .30038,31430. .31621,32179. .32262,32296. .32496,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(25014. .25018,25374. .25602)
/gene="JJ1118_B03.8"
/join(25014. .25018,25374. .25602)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAMPMVGVAPLMLSPVTMQAQLLCYVAMPMAPVAGGGVPLAAALCRLRNGTLERMMRE
MAQECTPPLVARRDRKSGATPPPPPPWWPTAEEPWWGTEVAAHLRGRRMATPVPFASP
RRLAKAEKVAVLVAVVRHVAPDFGRLAAAAGRSRLTELESSIWESALRGERERRYVVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="0J1118_B03.7"
/note="hypothetical protein
predicted by GlimmerM etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BAC06917.1"
/db_xref="G1:22093621"
/db_xref="G1:22093621"
/tanslation="MDAGSASCRESILGPCAACVRPRRAWPRLTRAGROEGEEAALAG
/translation="MDAGGGGGEGDGSEERRGRLLRRLRPVVAERIGNKDYILCVILVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAC06916.1"
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/translation="MKMTQGDIHLQAAGALDGEASIAGPATTGECAWMATRSCAALTA
LVQRLVRCGRASQFDPATDKIYKQQINKPIGCQADGAIPADADTSR"
                                                                                                                                                                                                                                                                                                                                                                                                             predicted by FGENESH etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predicted by GENSCAN"
join(29910. .30038,31430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="This category is not included in IRGSP standard.
hypothetical ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YDEVLRGLDELEIPSFFGGYYI"
join(25014. .25018,2537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSF ILLPPPPPPPPQHAHSAESAAAHAGPEPESADQTAVDFSVSGEDTVTTGPELEQL
VGDGNGATVEGEGQKTEDSPVPPLLEQHGGEDHDHHRQHGGFSGEVSGAAPEDVDWFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="OJ1118_B03.7"
22328. .23398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predicted by GeneMark.hmm
                                                      /protein_id="BAC06919.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                     note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       32801. .32899,33193. .33231)
/gene="OJ1118_B03.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAC06918.1"
/db_xref="GI:22093622"
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                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="OJ1118_B03.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MASSSSGKRVSSSSTSSHQQHAKRRRRAPGDELSQTHGVARNAV/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="0J1118_B03.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MGVVKSPAVVFLVESDQLKKIYPEESEFNEDAESFFLVLQGLVS/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e="0J1118_B03.6"
8. .19714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome 1, B1156H12.26'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .31621,32179.
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                                                                                                                                                                                              .39950,40746. .40820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
AP004572/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
A gene with identity or significant homology to a proclassified based on the protein name to indicate the such as same name, 'putative-' and '-like protein'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sasaki,T.,
                                                                       accession no.
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 TGACTTCAGGTGGACA 241
                                                                                                                                                                    AL Submitted (19-DEC-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nlas.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
On Aug 16, 2002 this sequence version replaced gi:21623780.
Cenes were predicted from the integrated results of the following: GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH (http://www.softberry.com/), GeneMark.hmm (http://www.softberry.com/), GeneMark.hmm (http://www.tigr.org/tdb/glimmerm/glmr_form.html), RiceHMM (http://rgp.lna.affrc.go.jp/RiceHMM/), SplicePredictor (http://biolnformatics.lastate.edu/cgi-bin/sp.cgi), BLASTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGACTTCAATTGTACA 101539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                BLASTX. The genomic sequence was searched Protein database, nr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa nipponbare(GA3) genomic clone:P0668C05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AP004572.3 GI:22296450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Only in Database (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone:P0668C05
identified cDNA sequences using BLASTN with accession no. and RGP clone ID.
                                                                 RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTs represent the
                                                                                                                                  (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 142081
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/gene="OJI118_B03.11"
join(45022. .45585,48876.
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GYIRGGRALAVRPSGHHDVDADRAELRLILLGIPDHQRANPTHHRRLLLRSANTLERN
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SSSPPREEG POASAGGTSFTLKTIQIYEORPKYQAFMYWPYDPSAILMLEKRQLEVDR
VDSHAGREEELLPRRIAARRALADYDSIOLYDQORGOFTLHKGLMKREIFYKYTOHME
REKSKQQKIEKRAKTCIPYCLLPPNTRTSQFTCRPIEESQEKKQEIGKEHCAEPRNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLKKKPKEAVTTEEKVTEPGEKQLSPNPPNRVTSNRESGTTKGKKRLPGGEQHTPTPK
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/db_xref="GI:22093624"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.5%;
72.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome 7, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 108992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                              the corresponding DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .51950)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .51950)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLN 17-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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protein is

A gene without

homology level

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FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SdC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRCSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.

The orientation of the sequence is from T7 to SP6 of the PAC clone. This sequence of P0668C05 clone has an overlap with OJ1118_B03 (DDBJ:AP003740) clone at the 5' end. Detailed information on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://rgp.dna.affrc.go.jp/GenomeSeq.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          overlap and assembly quality together with annotation of this entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is available at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #428. .8715, 8759. .9361)
//gene="00668C05.1"
Join(3987. .4160
8428. .8717
                                                           /gene="P0668C05.4"

Join(24628. .24657,25452.
/gene="P0668C05.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mmmDHNILIPLYSSLMMLVLGPLIIDVISVSNKIGRLFSAIARF LAHDDSVINSVVGNKIGRLFSAIARF LAHDDSVINSVVDNDPPSSQLLGGVVSCFDAMTVTTRLGLEWQRSGEAAMECQGCD IPMDATVDELLDRKWASEGELKDAFVFVFDRNEDGFICASELWSVMRRLGFKEGGVYED CMRMIHTFDEDRDGRISYLEFRRMMEDADGCALYFGIEGVLVILSTGVCGERAAVGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(12582...13145,16436...16490,19473...19510)
/gene="p0668C05.2"
join(12582...13145,16436...16490,19473...19510)
/gene="p0668C05.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="BAC10217.1"
/db_xref="GI:2236451"
/db_xref="GI:2236451"
/translation="MSAITTELLVLDDAAAGASKAAPGTGEARAAPDDRHHRRPPRST
/translation="MSAITTELLVLDDAAAGASKAAPGTGEARAALLLEKROLPVDR
SSSPPREEGPDASAGGTSFTLKTIQIYFQRPKVQAFMVWPYDPRAILMLEKROLPVDR
SSSPPREEGLERRATAARRALDDTDSINOYDQRGGFFLHKGLMKREIFYKTQHME
REKSKQOK LEKRAKTCIPYCLLPPNTRTSQFTCRPIEESQEKKQEIGKEHCABPRNL
REKSKQOK LEKRAKTCIPYCLLPPNTRTSQFTCRPIEESQEKKQEIGKEHCABPNRL
REKSKQOK LEKRAKTCIPYCLLPPNTRTSQFTCRPIEESQEKKQEIGKEHCABPNRL
ROSAGIELVLTKSQELSHYKESRNADMPRTQIRLGGRRRRGSAARWFATGGRSRGGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                   Juin(21422. .21505,21590.
/gene="P0668C05.3"
inim/olion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYIRGGRALAVRPSGHHDVDADRAELRLILLGIPDHQRANPTHHRRLLLRSANTLERN
TLKKKPKEAVTTEEKVTEPGEKQLSPNPPNRVTSNRESGTTKGKKRLPGGEQHTPTPK
/note="This category is not included in hypothetical ORF"
                                                                                                                                                                                      RDAARESALREIKERIKKTKDEKKAKKAEVAKSQKASGKGNAPKPGKGPKLGGGGGKR
                                                                                                                                                                                                                                                             /product="putative 60S ribosomal protein L24"
/protein_id="BAC10219.1"
/db_xref="GI:22296453"
                                                                                                                                                                                                                                                                                                                                                                                             join(21422 . 21505,21590 . .21691,21971 . .22119,22452.
/gene="P0668C05.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VQQQRMKTAHPQDGLTSTDSGTEDDKQQRPPARASHQRRGDNTNPKRTRKTQKSQQGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            predicted by FGENESH etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="P0668C05.1"
                                                   join(24628. .24657,25452. .25481,26190.
/gene="P0668C05.4"
                                                                                                                                                                                                         /translation="myrtelcresgakiypgkgirfiradsqyflesnskckryfhnr
LkpaklTwTamyrkqhkkdihaEavkkrrrTtkkpySRSIVGATLEVIQKkraEkpey
                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="BAC10218.1"
/db_xref="GI:22296452"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   predicted by GlimmerM etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                       note="contains ESTs D23260(C2515),C98364(C2515)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3987. .4169,6437. .6535,7385.
.8715,8759. .9361)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .6535,7385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .21691,21971.
                                                                                                                                  .25481,26190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .7510,8306. .8380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .7510,8306. .8380
                             IRGSP standard
                                                                              .26322,27451. .27491)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .22119,22452.
                                                                                                                                  .26322,27451. .27491)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 22599)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_teature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(28528..285/gene="P0668C05.join(28528..285
                                                                                                                                                                                                                                                                                        /protein_id="BAC10222.1"
/db_xref="GI:22296456"
/db_xref="GI:22296456"
/translation="MSIVLPILHURKELEFLNVRDASVGMLHMSIPHLATAARFDHRS
/translation="MSIVLPILHURKELEFLNVRDASVGMLHMSIPHLATAARFDHRS
VIGQSKIVLLPTULNQIAISSMEGGLEDTFPAANSEI"
join(66254__66289,67073. .67201,67242. .67324,68430. .6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(55139. .55378,60225. .60296))
/gene="P0668C05.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(55139. .55378,60225.
/gene="P0668C05.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(63541. .63724,63791. .63849))
/gene="p0668C05.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(63541. .63724,63791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="hypothetical protein predicted by GeneMark.hmm e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BAC10220.1"
/db_xref="GI:22296454"
/translation="MpDaAARPSAPGCRRSGTGPAAIAPHGPGRCRPSPAQARPPPPP
PGMAPPPLPLLGTGPAAAAPAQHGPGRCLGCFSRRSEEEKRGKLDQMWKRKGRGRDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(45109. .45453)
/note="5' LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="probably inactive due to frameshift(s) in CDS probably inactive due to stop codon(s) in CDS pseudogene, gypsy/Ty-3 retroelement polyprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(40452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(40109. .40452)
/note="3' LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(30351. .30405,31104. .31280,31382. .31464))
/gene="P0668C05.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(30351.
/gene="P0668C05.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="megtrrhlekdlepwriiedvQvkrveteAmAttleeeggrgvga
wralepeaeAaegkgggGADAgggTavGvnSTgrrgwgwegLggwedGAggwLDkvvg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predicted by GlimmerM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50849.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="P0668C05.7"
/note="rrc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(40452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   predicted by GlimmerM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="This category is not included in IRGSP standard.
hypothetical ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predicted by GENSCAN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="This category is hypothetical ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Join(28528. .28547,28852. .28939,29391.
/gene="P0668C05.5"
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rsavTgGRYGRARTAAASGGRVRPRQAAAFYGSDDQQVMLWMDRSKVRSSMTSSSVLS
                                                   /protein_id="BAC10223.1"
/db_xref="GI:22296457"
                                                                                                                                                        /gene="P0668C05.11"
                                                                                                                                                                                                              join(66254.
                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="hypothetical ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="P0668C05.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BAC10221.1"
/db_xref="GI:22296455"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="P0668C05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               predicted by GENSCAN"
                                                                                                                               /note="hypothetical ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="P0668C05.8"
                                                                                                                                                                                                                                       'gene="P0668C05.11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="P0668C05.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /pseudo
                                                                                                                                                                                         69007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .28547,28852.
205.5"
                                                                                                                                                                                                              66289,67073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .30405,31104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not included in IRGSP standard.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .28939,29391.
                                                                                                                                                                                                                 .67201,67242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .31280,31382.
                                                                                                                                                                                                              .67324,68430. .68550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .29495)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .29495)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .31464))
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JOURNAL REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (26-JAN-2002) Clemson University Genomics Institute Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (25-MAY-2001) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa chromosome 10 clone OSJNBa0004E08, complete sequence.
Wing.R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H., Rambo,T., Saski,C., Henry,D., Oates,R., Simmons,J., Wilson,R., Minx,P.,
                                                                                                                                                                                Wing,R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H.-R., Rambo,T.,
Saski,C., Henry,D., Oates,R., Simmons,J., Wilson,R., Minx,P.
                                                                                                                                                                                                                                Clemson University, 10
5 (bases 1 to 158294)
                                                                                                                                                                                                                                                        Submitted (01-FEB-2002) Clemson University Genomics Institute. Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wing, R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clemson University, 10 3 (bases 1 to 158294)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wing,R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H.-R., Rambo,T., Saski,C., Henry,D., Oates,R., Simmons,J., Wilson,R., Minx,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saski,C., Henry,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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70724. .70885
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/db_xref="GI:22296458"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yu,Y., Soderlund,C., Chen,M., Kim,H.-R., Rambo,T., Henry,D., Oates,R., Simmons,J., Wilson,R., Minx,P.
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                                                                                                    Institute,
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                                                                                                                                                                                                                                     repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-FEB-2002) Clemson University Genomics Institute,
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative TNP2-like transposable element"
/protein_id="AAL75729.1"
/b_xref="GI:18542887"
/tb_xref="GI:18542887"
/tanslation="MYNA2887"
TATWRGKMYKPVVIGLCGKALALLMDROWMYADRRSKEFIHGVHYFLRVAEANRORGF
TCCPCNKCKNQKEYSASRTIHFHLFESGFMPSYNCWTSHGEQGVEIEBDEVEDDNIPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Putative cyclophilin"
/protein_id="AAL75728.1"
/db_xref="GI:18542886"
/ta_nslation="MAPAASSKSNPRVFLDTAIGGEMVGRVVIELLADKVPDTAENFR
RLCTGERAGRSGKSRLHYKGSAFHRVVPGFMCQGGDITAGNGTGGESALDGAARHFPD
EGFAVKHDGPGVVSMANAGPNTNGSQFFITVDKAPWLDGRHVAFGRVVAGMGAVRAID
                                                                                 /note="Unknown protein" 22772. .23155
                                                                                                                                                                                   element"
                                                                                                                                                                                                        16649. .21066
/note="Contains similarity
                                                                                                                                                                                                                                                                                                                                       FRKAHFTVLQHSSLVAPYIEEHLALVRARNIGKSDAWITRHHIDTFPAWLRQHLMGNE
SINQQLAFLARGPSGSIATFQGYEINGYTFYTRAQDMKSTNQNSAVRVDAMGHDGTTA
                                                                                                                                                                                                                                                                                                                                                                                         QCLVSFEL1FPPSFFN1MTHLLCHLVKE1R1LGPMYLHNMFPFERYMGVLKKYVRNRA
RPEAS1AKGYGTEEV1EFCVEF1EDLRP1GVPESRHEGRLRGKGTLGRKAIMTVDNNL
                                                                                                                                                                                                                                                                                                                                                                                                                                         IFWELPYWEFLDVRHAIDVMHLTKNLCVNLLGFLGVYGKSKDTLEARNDLKHMEQRGD
LHPEPKEKGSHYLSPASYTLSKAEKESMFECLESIKVPSGYSTNIKLIISMKEKKFTN
LKSHDCHVLMTQLLPVVIRGILPDNVRATITKLCAFMNAISQKVIDPDRLEALQNEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIPAKVMWYFPIIPRLRRLFRNKGNAGMLRWHAEERQQDGMLRHPADGSQWRNIDRKF
KEFGKDARNIRFGPKQPGNDIDYYLRPLVEDLKQLWKKEGVPVWDEDKQEEFNLRALL
FVTINDWPALSNLSGQSNKGYKACTHCMDETESTYLKHCRKVVYMGHRRFLAANLPVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAQYVGFEGNQTGEEEIAADGNDVADDLGQMLQDAREDCESEKEAHKLDKMLEDHRTS
LYPGCEQGHKKLDTTLELLQWKAKNGVSDKAFGDLLKLVKNILPGGNKLPETTYEAKK
IVCPLGLEVHKIHACPNDCILYRGEEYENLEACPVCKALRYKIRRDDPGEVDGQLTKK
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                                                                                                                                                           22772. .23155
                                                                                                                                                                                                                                                                                                                  TYYGAIEDIWELDYGPLKVPLFRCQWVRLTGGGVMIDDSGMTTVVLNKVGYSDEPFVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKGKHFEHKADHHTKPKHRSGKTVFAMVKDLKVVFGKGPGSQHIESEDGHAAMWKKNS
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/chromosome="10"
                                                                                                                                                                                                                                                                                       ANDVTQVFFVKDMSRKGKKGRGPDEPKRQVVLPTKEKSSELRTRLTRITISWMGNPLI
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/note="Contains similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
     /product="Unknown protein"
                                                       /gene="OSJNBa0004E08.3"
                                                                                                                                 /gene="OSJNBa0004E08.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Contains similarity to TNP2-like transposable
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                                                                                                                                                                                                                                                                                                                                                                                                             /product="Hypothetical protein"
/protein_id="AAL/5732.1"
/protein_id="AAL/5732.1"
/db_xref="Gi:18542890"
/tränslation="MARWPAFSSSSAAASTARLRARRGGDDHICGYAEGSLSLVAHPT
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GLARVACAATRLSAAGTKSAVRVMHAMARHSATPAVLQEMLAVGVGARLLFLVQVGAS
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IGARIRDTDFLQGDDILWINFRGIYELYQLDALDVSIMSCWILMEIQRARRRRVFDTG
FIDPRKVNVAMLDQYPQETEDNLVHLLKAQHYKTFILLRYNTEFHWYLLLFDLEACTV
                          HGAGDVHPYVLELTSPSGKYAAYFVRSHTVPGAGGLGADFCYVEVVVNKGGEGDAAVA
AGGGMSVWESECRPVSTVNTCTLLFSWHGLEVFDGSQEVWHGETNTDGTNFLQRLELV
DDGDMRIRDKDGELAWRASDEPRHAQHCGAPGSPGLATAFPFEAFIGAHSSDLPFGM
FPGGNGRAAELPQAADAAAGALGGVGAVAPLPGAVGGAGAVAPLPGAAGGDAAAAPLP
                                                                                                                                                                                                                                                                                                                                                                                          GEQTRARASNVLARWDLGTGGNNFLGHEFTGLYRTRSPGQFVRK"
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PSPPHAPPAPSPPQAPASTPDAPTPPPPQAPPPPSPSKRAPPAPPPPAHT
RATKKAKVDAAKNKDPGYDCTQELLDAYVASEVYKRQFKPRSPEKKIPLDPSVRNEFER
MSASVKEAIKLSDYERTLKKASSGKSKPVPQLGEQPNQEIEPLVTGKENTIEQFITDT
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EEVARKVDERMAAHRSHDPQPTIPPAMVSPSGNRSSCASTGQVGSQSMDAMQTQDEST
CPVDDITQRTPCELHIPFKNLSIKVASGMAIPTDPSGTYHCRPIPAGYSKVEVELVEG
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TLPAGTEDKVKRWTLKKMAEQFQSFKGDMYQKYILKGQTPNFDTFPKLRDHWDEFIAY
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                                                                                                                                                         /product="Unknown protein"
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/db_xref="GI:18542891"
                                                                                                                                                                                                                                                                                           33040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="Hypothetical protein"
join(29297. .29344,29819. .30102,30427.
/gene="053108a0004E08.5"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVYDSMDKKESTFDKVFELIDRAWYRFRHLVRGKWRERLRRKFKFPCTKQKQGTNLCG
YYVCEYCHCLADQIITTRELDFIRMRDNLTTHKEFIAAVQEQLMGFINEEILDPKGEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(24059. .25480,25555. .26654,26764. .2
27229. .27301,27396. .27494,27574. .27759)
/gene="OSJNBa0004E08.4"
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NRRPDAATPPLTNENENDRTNESGNEHVNVRCRENVNENENDRTNESENENDRSKTSE
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                                                                                                                                                                                                                                                           /gene-"OSJNBa0004E08.6"
                                                                                                                                                                                                                                                                                                                /note="Unknown protein"
                                                                                                                                                                                                                                                                                                                                          /gene="OSJNBa0004E08.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="OSJNBa0004E08.5"
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/note="Simple Sequence Repeat (TA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="Putative TNP2-like transposable element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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TGAACTTGTGGTGCTCTGCACCCTAATTATTGCTCAGATGTGGCAATGGAGCTTCTATATT 123
                                                                                  GCCCGGGCTCACCAACTGGTTATGGAGGGGTTCAAGTACCATTTTCCTGA-AAAGGACGT 761
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GGCCGGGCTCACCAGCTGGCCCAGTGAAGGCTTAAAGACATGTGCCAGGAGAAGGGGCCT 63
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                                                                                                                                                                                                                       PI YOSHIE 1
PC C12N15//
C12R1:865),
PC C12N15//
CC Strandec
CC Topolog;
FH Key
FT CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OS Saccharomyces cerevisiae
PN JP 199042090-A/1
PD 16-FEB-1999
PF 29-JUL-1997 JP 1997203652
PR SHUN HARASHIMA, YOSHINOBU KANEKO, AKIO OGAWA, YUKIO MUKAI, TETSUJI TOMITA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     methods for preparation and utilization thereof Patent: JP 1999042090-A 1 16-FEB-1999; SHOWA SANGYO CO LTD, KANEKA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 936)
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                                    Conservative
                                                                                                                                                                                                                                                          Topology: Linear;
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                                                                                                                             /db_xref="taxon:4932"
189 c 233 g
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complement(34686, .35039)
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                                                                                                                                                                 /organism="Saccharomyces cerevisiae"
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                                  Score 40.4; DB Pred. No. 0.64; 0; Mismatches
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Matches 85; Conserv
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                                                                                                                                                      TGTAACCGTGTGGTCCGCGCCAAATTACTGTTATAGATGTGGTAATGTCGCGAGTGTAAT 1278
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1 (bases 1 to 1978)
Arndt, K.T., Styles, C.A. and Fink, G.R.
A suppressor of a HIS4 transcriptional defect encodes a protein with homology to the catalytic subunit of protein phosphatases cell 56 (4), 527-537 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae protein phosphatase catalytic subunit homologue (SIT4) gene, complete cds.
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QTPVFVGGD1HGQFHDLLELFRTAGGFPDD1NYIFLGDYVDRQYYSLETFTLLMCLKV
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KYPAKYCGD1HGQFHDLLELFRTAGGFPDD1NYIFLGALMGTKI
LCVHGGLSPEIRMLDQ1RYLSRAQEVPHEGGFSDLLMSDPDNVEAWQVSPRGAGWLFG
SKVAREFNHVNGLNLIARAHQLVMEGFKYHFPEKDVVTVWSAPNYCYRCGNVASYMKV
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/protein_id="AAA56864.1"
/db_xref="GI:598433"
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/db_xref="taxon:4932"
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query Match	Query Match Length DB	DВ	ID	Description
ר	223.4	55.6	1444	21	AAC46559	Zea mays DNA fragm
ν	93.6	23.3	1388	21	AAC47854	Arabidopsis thalia
ω	91.4	22.7	1310	21	AAC47706	Arabidopsis thalia
4	91.4	22.7	1311	21	AAC38705	Arabidopsis thalia
5	89.2	22.2	1083	21	AAC50898	Arabidopsis thalia
0	86.8	21.6	912	24	ABN85631	Protein phosphatas
7	40.4	10.0	936	20	AAX15651	Protein phosphatas
œ	37.2	9.3	252	14	AAQ36833	Leu8 hPTH mutein g
ი 9	37.2	9.3	2413	23	ABV25283	Human prostate exp

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		n control;	Genomic sequence # Genomic sequence # Genomic sequence # Staphylococcus aur	Candida tropicalis Candida tropicalis Human polynucleoti Partial mouse WRN Genomic sequence #	Tunour suppressor Chemically treated Signal transductio Staphylococcus epi Human brain Expres Human immune/haema Human immune/haema Enterococcus faeca	Gene for Cys35 hpT Gene for Cys35 hpT Met18 hPTH mutein Leu8, 18 hPTH mute Human parathyroid Parathyroid hormon Human neuroblastom Human lung tumour- Drosophila melanog Human cervical can	Human nGPCR-Seq102 Human G-protein co Human G protein co Human G protein co Pyrococcus abyssi Gene for hPTH mute Gene for hPTH mute Gene for hPTH mute Gene for hPTH mute

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                     Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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99US-0123548.
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Best Local Similarity 72...
Matches 162; Conservative
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                                                                                                                                             AGCTTCGATGAGAAGAAGAAGGAGATGTCAAGGTCTTCACAGAGACCGAGGAAAACAA 184
                           (first entry)
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72.3%;
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Capathway: promoter; termination sequence; Ss. siz thaliana  5-AZ  000, 2000EP-0301439.
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RESULT 4
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70.4%;
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Best Local Similarity 70.4%;
Matches 164; Conservative
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PR 18-JU PR 23-JU PR 113-JU PR 23-JU PR	04-JUN-1999; 99US-013750 07-JUN-1999; 99US-013809 10-JUN-1999; 99US-013809 10-JUN-1999; 99US-013814 14-JUN-1999; 99US-013945 16-JUN-1999; 99US-013945 16-JUN-1999; 99US-013945 17-JUN-1999; 99US-013945 18-JUN-1999; 99US-013945 18-JUN-1999; 99US-013945 18-JUN-1999; 99US-013945 18-JUN-1999; 99US-013945 18-JUN-1999; 99US-013945 18-JUN-1999; 99US-013945 18-JUN-1999; 99US-013945 19-JUN-1999; 99US-013945	Arabidopsis thaliana DNA fragment SEQ ID NO: 66541.  XX Hybridisation assay; genetic mapping; gene expression control;  XW Hybridisation assay; genetic mapping; gene expression control;  XW Protein identification; signal transduction pathway;  XW protein identification; signal transduction; signal transduction pathway;  XW protein identification; signal transduction pathway;  XW protein identification; signal transduction pathwa	SULT 5 C50898 AAC50898 standard; D AAC50898;
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70.9%;
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                                                                                                                                             Query Match
Best Local S
Matches 146
                                                                                                                                                                                                                                                                                                      WPI; 200
P-PSDB;
                                                                                                                                                                                                                   The invention relates to a nucleic acid molecule (ABN85631) encoding catalytic subunit of protein phosphatase 2A (ABB83820) that regulates flowering timing in plants is provided, thereby delaying flowering times.
                                                                                                                                                                                                                                                                                                                                  Kang
                                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                          Nucleic acid molecule encoding catalytic subunit of 2A that regulates flowering time in plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                     19-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                       19-OCT-2001; 2001KR-0064613.
                                                                                                                                                                                                                                                                                                                                                                                                          29-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                            KR2001106331-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein phosphatase 2A catalytic subunit encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABN85631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABN85631
                                                                                                                                                                                                                                                                                                                                                   (KOKU-)
870
                                                                                                           692
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                                                                                                                                             Local Similarity
les 146; Conserv
                                                                                                                                                                                                   plants
aves of
                                                                                                                            σ
                                                                                                         CCAGATTCCAGGGCCAAGGGCTTGGA
                                                                                                                                                                                                                                                                                                                                  JG,
TCAGATGAGAGGGCCAAGGACAGGTGTTCC
                                                                      CCAGATTCCAGGGCCAAGGGCTTGGAATCC
                                                                                                                                                                                                                                                                                                      2002-349593/38.
DB; ABB83820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAAATGAGAGGGCCAAGGACAGGTA
                                   {f AGTTTCAATGAAAATATGGAGA-GAGAAGTTAAGTTTTTCACTGAAACAGAGGAGAACAA}
                                             AGCTTCGATGAGAAGAAGGAAAGGAGATGTCAAGGTCTTCACAGAGAGACCGAGGAAAACAA
                                                                                       GAACTTGTGTGGTCTGCACCCTAATTATTGCTCAGATGTGGCAATGGAGCTTCTATATTA 124
                                                                                                                                                                                                                                                                                                                                                   KOREA KUMHO PETROCHEMICAL CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; DNA; 912
                                                                                                                                                                                 912 BP;
                                                                                                                                                                                                                                                                                                                                 Park CM,
                                                                                                                                                                                                   and transferring nutrients effectively to roots, stems and crops.
                                                                                                                                                                                                                                                        Fig 2; 19pp; Korean.
                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                      2001KR-0064613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                           /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1..912
/*tag= a
                                                                                                                                                                                 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2A; enzyme;
                                                                                                                                                                                                                                                                                                                                  Song
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                    21.6%;
                                                                                                                                                                                A; 170
                                                                                                                                                                                                                                                                                                                                  PS;
                                                                                                                                                                                                                                                                                                                                                                                                                                            "Protein
                                                                                                                                              0;
                                                                                                                                                                                C; 207 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                             Score 86.8; DB 24;
Pred. No. 2.9e-18;
0; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plant; flowering; crop;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210
                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphatase
899
                214
                                                                                                                                                                                278 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                              2A
                                                                                                                                                              Length
                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             catalytic
                                                                                                                                                                                                                                                                                   protein phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene;
                                                                                                                                                               912;
                                                                                                                                                                                                                                                                                                                                                                                                                                             subunit"
                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ds.
                                                                                                                                             Gaps
                                                                                                                            64
                                    869
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RESULT 8
AAQ36833
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AAX15651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 85
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a protein phosphatase gene sequence of Saccharomyces cerevisiae. The specification describes new of Saccharomyces cerevisiae in which the growth and/or the fermentation activity is controlled at least in the range of 0-20 degrees Celsius. These yeast are prepared by deleting the function of at least one protein the protein that the prepared by deleting the function of at least one protein the protein that the prepared by deleting the function of at least one protein the protein that the prepared by deleting the function of at least one protein the protein that the prepared by deleting the function of at least one protein the protein that the prepared by deleting the function of at least one protein the protein that the protein the protein that the protein the protein that the protein that the protein that the protein the protein the protein that the protein the protein that the protein that the protein the protein that the protein that the protein the protein that the protein the protein that the protein the protein that the protein that the protein that the protein that the protein the protein that the protein th
                                     Human parathyroid hormone; hypercalcaemia; ss.
                                                                                                                          09-JUN-1993
                                                                                                                                                         AAQ36833;
                                                                                                                                                                                         AAQ36833 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP11042090-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein phosphatase gene; growth; dough production; yeast; ds.
                                                                                        Leu8 hPTH mutein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 936 BP; 261 A; 189 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 16-17; 41pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX15651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX15651 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphatase gene. The yeast is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New yeast of controlled activation at low temperatures -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Improving the quality of dough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KANF ) KANEKA CORP.
(SHOS ) SHOWA SANGYO CO
                                                                                                                                                                                                                                                                         822
                                                                                                                                                                                                                                                                                                          124
                                                                                                                                                                                                                                                                                                                                          762
                                                                                                                                                                                                                                                                                                                                                                                                         703
                                                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                              AAGCTTCGATGAGAAGAAGGAA 145
                                                                                                                                                                                                                                                                                                                                                           TGAACTTGTGTGGTCTGCACCCTAATTATTGCTCAGATGTGGGCAATGGAAGCTTCTATATT
                                                                                                                                                                                                                                                                                                                                                                                                         GCCCGGGCTCACCAACTGGTTATGGAGGGGGTTCAAGTACCATTTTCCTGA-AAAGGACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCCGGGCTCACCAGCTGGCCCCAGTGAAGGCTTAAAGACATGTGCCAGGAGAAGGGGCCT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1999-197822/17
                                                                                                                                                                                                                                                                         GAAGGTCGATGAGGATCTGGAA 843
                                                                                                                                                                                                                                                                                                                                        TGTAACCGTGTGGTCCGCGCCAAATTACTGTTATAGATGTGGTAATGTCGCGAGTGTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
                                                                                                                        (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97JP-0203652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97JP-0203652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                         DNA;
                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene coding sequence of Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.0%;
59.9%;
                                                                                                                                                                                           252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    936
                                                      hPTH; antagonist; hypoparathyroidism;
                                                                                                                                                                                           ΒÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40.4; In Pred. No. 0.00 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful in the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fermentation activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        one protein of dough.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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                                                                                                                                                                                                                                                                                                                                        821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                        밁
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ABV25283/c
ID ABV25283 standard;
                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
WO200160860-A2
                                                         Human; prostate pharmacogenomic
                                                                                                      Human prostate expression marker cDNA
                                                                                                                                                                    ABV25283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        absorption by tissue
can be used as a the
hyperparathyroidism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hormone (hPTH) where Met8 is substd. by Leu. The peptide can have higher stability, enhanced activity and improved absorption by tissues. It can act as a PTH antagonist and can be used as a therapeutic agent for hypercalcaemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human parathyroid mutein(s) - osteoporosis, hypoparathyroidism, hypercalcaemia, hypertension etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-1991;
26-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                            Homo sapiens
                                                                                                                                      16-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of a gene coding for human hormone (hPTH) where Met8 is substd. by Leu. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-060187/08.
P-PSDB; AAR30858.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fukuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Page 21; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-FEB-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP528271-A.
                                                                                                                                                                                                                                                                             198
                                                                                                                                                                                                                                                                                                            185
                                                                                                                                                                                                                                                                                                                                          138
                                                                                                                                                                                                                                                                                                                                                                     125
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                                                                                                                                                                                                                                                                                                                                                                                                                                  65
                                                                                                                                                                                                                                                                             გ=
                                                                                                                                                                                                                                                                                                                                                                                                                     GAACTTGTGTGGTCTGCACCCTAATTATTGCTCAGATGTGGGCAATGGAGCTTCTATATTA 124
                                                                                                                                                                                                                                                                                                          CC 186
                                                                                                                                                                                                                                                                                                                                          TGGTTCCCAAAGACCACGTAAAAAGGAAGACAATGTCTTAGTTGAGAGCCATGAAAAATC 197
                                                                                                                                                                                                                                                                                                                                                                    AGCTTCGATGAGAAGAAGGAAAGGAGATGTCAAGGTCTTCACAGAGACCGAGGAAAACAA 184
                                                                                                                                                                                                                                                                                                                                                                                                   GAAGTTGCAGGATGTGCACAATTTTGTTGCCTTAGGTGCCGCATTGGCTCCTCGTGATGC 137
                                                                                                                                                                                                                                                                             199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 BP; 72 A; 53 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                    (first entry)
                                                           marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91JP-0198056
92JP-0169713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92EP-0113322
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19..24
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/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1..252
                                                                                                                                                                                                  cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.38;
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                                                           gene;
                                                                         cytostatic;
                                                                                                                                                                                                  2413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37.2;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 G; 62 T; 0 other;
                                                            SS
                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leu-Met ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hyperparathyroidism,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for treating e.g.
                                                                         carcinogen;
                                                                                                         25274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTG CTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53;
                                                                         pharmacodyanamic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parathyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leu-Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                           marker;
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ARESULT 10
AREJOA44/
ID AREJOA44/
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XX AREJOA
XX Huma
XX Huma
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XX Anti
KW Anti
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                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of t specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                               patient;
(I) is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-FEB-2000;
16-MAR-2000;
                     Human; G protein-coupled receptor; GPCR; nGPCR; vulnerary; antiasthm anti-HIV; analgesic; cytostatic; antidiabetic; anorectic; metabolic; hypertensive; hypotensive; thrombolytic; antiparkinsonian; cardiant;
                                                                                                                                                                                                                           2115
                                                                                                                                                                                                                                                                                                                                 2235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated prostate cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (f) (d)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for
             antiatherosclerotic;
                                                                                                        18-JUN-2002
                                                                                                                                 ABL50444
                                                                                                                                                           ABL50444 standard;
                                                                                                                                                                                                                                                                                                                                                        217
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (d)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schlegel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MILL-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  el isolated nucleic acid molecule associated with cancerous stat
state cells and correlating with presence of prostate cancer, us
detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     selecting a composition for inhibiting prostate cance assessing the prostate cell carcinogenic potential of determining whether prostate cancer has metastasized assessing the aggressiveness or indolence of prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      assessing the efficacy of a therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            patient;
                                                                                                                                                                                                                           CATTTCCATTTTAGCTTTTTTAAAAAAACAAAAAGCTGTTGTGGACAGATGAACATCC
                                                                                                                                                                                                                                                CATTTCTGGTTTCTTTTGAACACAAGTACAAAAAAACCAACGGGAGGGGCATAACTTCC
                                                                                                                                                                                                                                                                             TTATACAATGAACATGTATTAATTGTAGAAGAAAACGATGTCATCCTTTATGATAAAATC
                                                                                                                                                                                                                                                                                                     AAGAACAATCAGATGGTGTTAATTGTGGAGGTTCAGATCATAATGCCATCTGATGCATTC
                                                                                                                                                                                                                                                                                                                              TATTTTTTTTTTTACCAGTAGTTCCTTTCCCGCTTTATTTTTTAGCTGCTTTTTGGGTT 2176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-662795/76.
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                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 4968; 11750pp; English.
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; 2000US-189862P.
; 2000US-207454P.
; 2000US-211314P.
; 2000US-2119007P.
; 2000US-255281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                     (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                     BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                      565
                                                                                                                                                           cDNA;
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MO
                                                                            polynucleotide
                                                                                                      entry)
             neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                               9.3%;
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                                                                                                                                                           1971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolated nucleic acid molecule (I) comprising
in Tables 1-9 (ABV00010-ABV62213) of the
ment. (I) is useful for:
                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                            Score 37.2;
Pred. No. 0
                                                                                                                                                           ВP
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                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     612 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JE;
            antimigraine; neuroprotective;
                                                                            sequence
                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                     576 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate cancer in a patient;
                                                                            SEQ
                                                                                                                                                                                                                                                                                                                                                                                  ; 88
                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                                                                                                                                                                                                                                                                                     9 other;
                                                                            ID NO:15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prostate
                                                                                                                                                                                                                                                                                                                                                                                                          Length
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                                                  antiasthmatic;
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cer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             state
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                   394
diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tate of
useful
cer -
            cancer;
                                                                                                                                                                                                                                                                                                     336
                                                                                                                                                                                                                                                                                                                                                        276
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03-MAY-2000;
03-MAY-2000;
03-MAY-2000;
03-MAY-2000;
03-MAY-2000;
03-MAY-2000;
03-MAY-2000;
03-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               human immunodeficiency virus; obesity; anorexia; hypotension; thrombo, hypertension; myocardial infarction; cardiomyopathy; atherosclerosis; Parkinson's disease; schizophrenia; migraine; anxiety; manic depression dementia; Huntington's disease; thyroid disorder; inflammatory condit rheumatoid arthritis; autoimmune disorder; hormonal disorder; psorias
                                                                                                                                                                                                                                  01-MAY-2001;
                                                                                                                                                                                                                                                                                    08-NOV-2001
                                                                                                                                                                                                                                                                                                                                       WO200183553-A2
                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                          renal failure; movement disorder; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiarthritic; immunosuppressive; antipsoriatic; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                       sapiens.
                                                                       2000US-201549P.
2000US-201550P.
2000US-201551P.
2000US-201552P.
                       2000US-201632P.
2000US-201633P.
                                                                                                                                                                                                                                  2001WO-US14050
                                                                                                                                                                                  2000US-201548P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               depression; ry condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombosis;
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polypeptides encoded Alzheimer's disease, Novel G anorexia protein-coupled receptor-x nucleic acid molecule and tides encoded by them, useful for treating cancers, psoriasis, er's disease, atherosclerosis, rheumatoid arthritis, obesity,

P-PSDB;

ABB06813.

2002-041488/05

Parodi

LA,

Lind

Þ,

Sejlitz G

н

(PHAA)

PHARMACIA &

UPJOHN

2000US-201978P

Claim 3; Page 70-71; 193pp; English.

CC antirheumatic, antiarprinting, municipally and antiportective, tranquilliesr, antidepressant, antiinflammatory, antirheumatic, antiarthritic, immunosuppressive and antipsoriatic activities. They can be used as immune response inducers, nGPCR CC expression or activity modulators and in gene therapy. nGPCR CC expression or activity modulators and in gene therapy. nGPCR CC polynucleotide sequences can be used as probes to screen databases and concleic acid libraries, for screening restriction fragment length complete complete complete companying nGPCR sequences can be used in the treatment of diseases such companying nGPCR sequences can be used in the treatment of diseases such cas viral infections caused by human immunodeficiency virus (HIV)-1 or CC at virus cancers, diabetes, obesity, anorexia, hypotension, thrombosis, myocardial infarction, cardiomyopathies, cardiorescis, parkinson's disease, existence anxiety, comanic depression, dementia, Huntington's disease, thyroid disorders, can inflammatory conditions, rheumatoid arthritis, autoimmune disorders, companying conditions, rheumatoid arthritis, autoimmune disorders, companying conditions, renal failure, psoriasis, movement disorders. (nGPCR) proteins given in ABB06799 to ABB06867. The nGPCR sequences have vulnerary, antiasthmatic, anti-HIV, analgesic, cytostatic, antidiabetic, anorectic, metabolic, hypertensive, hypotensive, antiatherosclerotic, antiparkinsonian, cardiant, neuroleptic, antiparkinsonian, neuroleptic, n ABL50430 to ABL50496 encode the human novel G protein-coupled receptor have

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Sequence
1971
BP;
652 A; 311 C;
374 G;
634 T;
0 other;
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Matches Query Match Best Local

Similarity

9.1%;

0; Score Pred.

Mismatches 36.4; DB No. 0.24;

Indels Length

Gaps

0;

DВ 61;

1971; 0;

밁 δÃ 151 211 246 ATGTCAAGGTCTTCACAGAGACCGAGGAAAACAACCAGATTCCAGGGCCCAAGGGCTTGGA ATAACAAGCTCTGGAAGAGTACAGAAGAATGACTACAGAGCCCCACGACGACAGTCTGGCA ATCCCATATTTCCTTTGACTTCAGGTGGACAATTTTAGAAGGCAATATTTAAATCTGGAA 270 187 210

Ъ QY 186 CAGAGACATACCCTTTGATTCGAGGTAGACATTAGCTGATGACATTTTTGTAATTTTGCA 127

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RESULT 11
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03-AUG-2000;
21-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; G-protein coupled receptor; GCREC-3; cell proliferative disorder; neurological; cardiovascular; gastrointestinal; autoimmune; inflammatory; metabolic; hepatitis; psoriasis; cancer; epilepsy; Alzheimer's disease; pick's disease; Huntington's disease; parkinson's disease; hypertension; atherosclerosis; myocardial infarction; gastritis; cirrhosis; cytostatic; osteoporosis; Crohn's disease; acquired immunodeficiency syndrome; AIDS; anaemia; asthma; rheumatoid arthritis; diabetes; obesity; drug screening; transgenic animal; allergy; gene therapy; hepatotropic; anticonvulsant;
                      useful for diagnosing, treating and preventing a cell proliferative disorder (e.g., hepatitis, psoriasis, cancer), a neurological disorder (e.g., epilepsy, Alzhaimer's disease, Pick's disease, Huntington's
                                                                                                                                                                                                                                                                                                        Thornton N
Elliot VS,
                                                                  The invention relates to novel human G-protein coupled receptors (GCREC) and their encoding polynucleotides. GCREC is useful as an immunogen for preparing monoclonal and polyclonal antibodies. GCREC
             disease,
                                                                                                                               Claim 5;
                                                                                                                                                           cardiovascular, gastrointestinal,
metabolic disorders -
                                                                                                                                                                                       New human G-protein coupled receptor polypeptide for diagnosis, prevention and treatment of cell proliferative, neurological,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virucide; gene;
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nootropic; neuroprotective; cardiant; immunosuppressive; anorectic;
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15-SEP-2000;
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                                                                                                                                                                                                                                                                                            AJA,
             Parkinson's disease),
                                                                                                                             Page 138-139; 150pp; English.
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                                                                                                                                                                                                                                                                           Warren
                                                                                                                                                                                                                                                                                                     Ramkumar J,
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2000US-232691P.
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2000US-227054P.
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                                                                                                                                                                                                                                                                                            Yao MG,
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                                                                                                                                                                                                                                                                             ΒA,
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J, Baughn MR, Kallick
Lu Y, Tribouley CM,
Lue EA, Ding L;
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             a cardiovascular disorder (e.g.,
                                                                                                                                                                         autoimmune/inflammatory, and
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                                                                                                                                                                                                                                                                                      DA, Walia I
Policky JL,
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myocardial

gastrointestinal

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Best Local S
Matches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier or affected individuals, and as hybridization probes for mapping naturally occurring genomic sequences. GCREC is useful in Southern or northern analysis, dot blot or other membrane-based technologies, in pck technologies, in dipstick, pin, multiformat enzyme linked immunosorbant (ELISA)-like assays, and in microarrays utilising fluids or tissues from patients to detect altered GCREC expression. The present sequence is human GCREC-3 cDNA.
                                                                                                                                                                                                                                                                                                    tumour growth; thyroid disorder; myxoedema; renal failure; inflammatory condition; Crohn's disease; cell differentiation; homeostasis; rheumatoid arthritis; autoimmune disorder; movement disorder; central nervous system disorder; stroke; Huntington's disease; Tourette's Syndrome; Parkinson's disease; Alzheimer's disease; viral infection; human immunodeficiency virus; Alzheimer's disease; viral infection; human immunodeficiency virus; HIV; metabolic disorder; cardiovascular disease; type 2 diabetes; obesity; hypotension; hypertension; thrombosis; myocardial infarctic atherosclerosis; proliferative disease; hyperproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorder (e.g., gastritis, cirrhosis, Crohn's disease), an autoimmune/inflammatory disorder (e.g., acquired immunodeficiency syndrome (AIDS), allergy, anaemia, asthma, rheumatoid arthritis), a metabolic disorder (e.g., diabetes, obesity, osteoporosis), and viral infections. GCREC is useful in a number of drug screening techniques, and to analyse the proteome of a tissue or cell type. GCREC is useful for creating knockin humanised animals or transgenic animals to model human diseases, in
                                    WO200179292-A2
                                                                                                                                                                                                                              nootropic; neuroprotective; cytostatic; antirheumatic;
cerebroprotective; anticonvulsant; neuroleptic; anorec
                                                                                                                                                                                                                                                                  psoriasis; hormonal disorder; polycystic ovarian syndrome; alopecia;
sexual dysfunction; respiratory ailment; asthma; brain injury;
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                                                                                                                                                                      sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein-coupled receptor (GPCR) nGPCR-1025 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein-coupled receptor; GPCR; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                              antiarteriosclerotic;
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                                                                  /product=
                                                                                          Location/Qualifiers
40..1329
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54.5%;
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                                                                        "Human nGPCR-1025 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
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                                                                                                                                                                                                                                anorectic;
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                                                                                                                                                                                                                                  cardiant;
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RESULT 13
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ID AAH412
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Best Local S
Matches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and for treating thyroid disorders (e.g., myxoedema), renal failure, inflammatory conditions (e.g., Crohn's disease), diseases related to cell differentiation and homeostasis, rheumatoid arthritis, autoimmune disorders, movement disorders, central nervous system disorders (e.g., stroke, Huntington's disease, Tourette's Syndrome, Parkinson's disease, Alzheimer's disease), infections, such as viral infections caused by HIV-1 or HIV-2 (human immunodeficiency virus), metabolic and cardiovascular diseases and disorders (e.g., type 2 diabetes, obesity, hypotension, hypertension, thrombosis, myocardial infarction, atherosclerosis), proliferative diseases and cancers, hyperproliferative disorders (such as psoriasis), hormonal disorders (e.g., polycystic ovarian syndrome, alopecia), and sexual dysfunction. nGPCR-1025 is useful and/or transmatth harby distances and for treating acute and/or transmatch harby allments such as asthma and for treating acute and/or transmatch harby allments such as asthma and for treating acute and and the contents and and contents acute and contents and contents and contents acute acute and contents acute 
                           Pyrococcus abyssi
                                                                        Hyperthermophilic archaeon;
                                                                                                                                                                       29-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor (GPCR) polypeptide, nGPCR-1025. nGPCR-1025 DNA may also be useful in gene therapy. The invention is used to treat or prevent unregulated cellular growth, such as cancer cell and tumour growth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid molecule encoding G protein-coupled receptor polypeptide, nGPCR-1025, useful for treating, e.g., cancer Crohn's disease, rheumatoid arthritis, Alzheimer's disease, stroke,
                                                                                                                        Pyrococcus
                                                                                                                                                                                                                                                                    AAH41224 standard; DNA; 349980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soderberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to an isolated nucleic acid molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thrombosis and psoriasis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 ATGTCAAGGTCTTCACAGAGACCGAGGGGAAAACAACCAGATTCCAGGGCCAAGGGCTTGGA 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGGTAAAGAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCCCATATTTCCTTTGACTTCAGGTGGACAATTTTAGAAGGCAATATTTAAATCTGGAA
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                                                                                                                abyssi genomic fragment #3
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                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                      hyperthermophilic
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                                                                      protein;
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nGPCR-1025
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RESULT 14
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                    Human parathyroid hormone; hypercalcaemia; ss.
                                                       Gene
                                                                            09-JUN-1993
                                                                                                  AAQ35228
                                                                                                                        AAQ35228 standard;
                                                                                                                                                                                                                                                                                                                                       Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CNRS )
                                                                                                                                                                                                    145
                                                                                                                                                                                                                                                                                                                   Sequence 349980 BP; 94090 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleotide sequences isolated proteins useful in industry -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-126236/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 347-443; 1657pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Querellou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-1999;
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                                                                                                                                                                                                   AAGGAGATGTCAAGGTCTTCACAGAGACCGAGGAAAA
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59; Conserver
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300001.349980
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/note= "This sequence overlaps with the
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1..49980
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/note= "This sequence
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                                                    lacking
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                                hPTH;
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                                                      6 N-terminal amino
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Pred. No. 3.8;
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                               antagonist;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  overlaps with the
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                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                      38;
                               hypoparathyroidism;
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                                                      acids
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RESULT 15
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mutation
                                       CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human parathyroid mutein(s) - osteoporosis, hypoparathyroidism, hypercalcaemia, hypertension etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                      Synthetic
                                                                                           hypercalcaemia;
                                                                                                     Human parathyroid hormone; hPTH;
                                                                                                                         Leu8 hPTH (7-84) mutein gene
                                                                                                                                               09-JUN-1993
                                                                                                                                                                                         AAQ36836 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 7; 88pp; English.
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P-PSDB; AAR30852.
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26-JUN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   therapeutic agent for hypercalcaemia and hyperparathyroidism
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                                                                                                                                                                                                                                                                                                                             GAAGTTGCAGGATGTGCACAATTTTGTTGCCTTAGGTGCCCCATTGGCTCCTCGTGATGC
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nilarity 55.7%;
Conservative
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92JP-0169713
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        /note=
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1..234
                           /*tag=
                                                Location/Qualifiers
                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "codes for peptide lacking N-terminal region"
                 "encodes mutein
                                                                                                                                                                                         ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                57 G; 58 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                    antagonist; hypoparathyroidism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hyperparathyroidism,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for treating
                 hPTH amino acids 7-84"
                                                                                                                                                                                                                                                                                                                                                                      54;
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Search completed: January Job time: 304 secs
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Matches 68
                                                                                                                                                                                                                                                                      The sequence is that of a gene coding for human parathyroid hormone (hPTH) amino acids 7-84 where Met8 is substd. by Leu. The peptide can have higher stability, enhanced activity and improved absorption by tissues. It can act as a PTH antagonist and can be used as a therapeutic agent for hypercalcaemia and
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26-JUN-1992;
                                                                                                                                                                                                                                       Sequence 234 BP; 70 A; 50 C; 57 G;
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                                                                                                                                                                                                                                                            hyperparathyroidism.
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                                                                                                         AGCTTCGATGAGAAGGAAGGAGATGTCAAGGTCTTCACAGAGACCGAGGAAAACAA 184
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DB; AAR30859.
                                                                                                                                          GAAGTTGCAGGATGTGCACAATTTTGTTGCCTTAGGTGCCCCCATTGGCTCCTCGTGATGC 119
                                                                                           TGGTTCCCAAAGACCACGTAAAAAGGAAGACAATGTCTTAGTTGAGAGCCATGAAAAATC 179
                                                                                                                                                                                       68; Conservative
                                                                     186
                                                181
                                                                                                                                                                                                                                                                                                                                             Page 21; 88pp; English.
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92JP-0169713
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Result
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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Listing first 45 summaries
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/B_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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                                         US-08-733-446-61
US-08-733-446-21
US-08-733-446-22
US-08-733-446-25
US-08-733-446-26
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US-08-733-446-26
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US-08-733-446-56
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US-08-733-446-31
US-08-733-446-31
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US-08-733-446-3
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US-08-733-446-19
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29.4	29.6	29.6	29.6	29.6	30	30.4	30.4	30.4	30.6	31	31	31	31.6	31.6	32	32	32.4
7.3	7.4	7.4	7.4	7.4	7.5	7.6	7.6	7.6	7.6	7.7	7.7	7.7	7.9	7.9	8.0	8.0	8.1
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Sequence 1614, Ap	Sequence 111, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 112, App	Sequence 1, Appli	Sequence 7, Appli	7,	Sequence 7, Appli	Sequence 134, App	Sequence 38, Appl			Sequence 20, Appl	Sequence 20, Appl	Sequence 1, Appli	Sequence 3, Appli	Sequence 209, App

#### ALIGNMENTS

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REFERENCE/DOCKET NUMBER: 4202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEPAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FUKUDA, TS
TITLE OF INVENTION: H
TITLE OF INVENTION: P
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NEUNER, George W
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/733,446
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: CUSHMAN
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                                                                      MOLECULE TYPE:
                                                                                       STRANDEDNESS: dou
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/926,787
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                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
IDENTIFICATION METHOD:
                                 NAME/KEY: CDS
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5. 5856138
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HUMAN PARATHYROID HORMONE
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                                                                      acid,
                                                                    synthetic DNA
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                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 4202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEPAX: (617)523-6440
TELEPX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 61, Appli
Patent No. 5856138
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                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/402.470
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                         FEATURE:
                                                                                                       MOLECULE TYPE: other nucleic acid, synthetic DNA
                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                           NAME/KEY:
LOCATION:
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                                                         NAME/KEY: CDS
LOCATION: 1..234
                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                      FILING DATE:
APPLICATION NUMBER: US/07/926,787
FILING DATE:
                                                                                                                       TOPOLOGY:
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              IDENTIFICATION METHOD:
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                                                                                                                                                                 234 base pairs
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                                         mutation
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HUMAN PARATHYROID HORMONE MUTEINS AND
PRODUCTION THEREOF
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                                                                                                                                                         TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 237 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 Patent No.
            Query Match
Best Local Similarity
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Best Local (
 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US
FILING DATE: 18-OCT-15
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FUKUDA, TO
TITLE OF INVENTION: I
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
                                                                                                                                                                                                                                                                                                                                                     FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                          FEATURE:
                                                                                                                                        MOLECULE TYPE:
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                                                                                        NAME/KEY: CDS
                                                                          LOCATION: 1..237
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: APPLICATION NUMBER: US/07/926,787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
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                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                      NAME: NEUNER, George
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). 5856138
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WENTION: HUMAN PARATHYROID HORMONE MUTEINS AND
 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.25
                                                                                                                                                     linear
                                                                                                                                                                                                                                                                             (617)523-3400
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              8.9%;
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0;
            Score 35.6; DB 2; Pred. No. 0.036;
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                            Length 237;
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US-08-733-446-21
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                                                              Matches
                                                                                            Query Match
                                                                                                                                                                                                                                                                                  TELEX: 200291 STRE UR INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                NAME: NEUNER, George W
REGISTRATION NUMBER: 26964
REFERENCE_DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                         MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435 PRIOR APPLICATION DATA:
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 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                    LENGTH: 240 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                TELEFAX:
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                                                                                                                                                           LOCATION:
                                                                                                                                                                          NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
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                                                                             Госа І
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GAAGTTGCAGGATGTGCACAATTTTGTTGCCTTAGGTGCCCCATTGGCTCCTCGTGATGC 125
                             GAACTTGTGTGGGCACCCTAATTATTGCTCAGATGTGGCAATGGAGCTTCTATATTA 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAACTTGTGTGGTCTGCACCCTAATTATTGCTCAGATGTGGCAATGGAGCTTCTATATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGTTGCAGGATGTGCACAATTTTGTTGCCTTAGGTGCCCCATTGGCTCCTCGTGATGC
                                                             . Similarity 55. 68; Conservative
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                                                                                                                                                                                                                                                                                                                                  (617)523-6440
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                                                                                                                                                                                                                          linear
                                                                                                                                                                                                        other nucleic acid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
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HUMAN PARATHYROID HORMONE MUTEINS AND
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                                                                            8.98;
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                                                           Score 35.6; DB Pred. No. 0.036; 0; Mismatches
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                                                                                                                                                                                                        synthetic DNA
                                                                                       DB 2;
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                                                                                         Length 240;
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                                                                                                                   Matches
                                                                                                                                              Query Match
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TELEPAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 243 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                       FEATURE:
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APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
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               125 AGCTTCGATGAGAAGAAGGAAGGAGATGTCAAGGTCTTCACAGAGAGACCGAGGAAAACAA 184
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129 TGGTTCCCAAAGACCACGTAAAAAGGAAGACAATGTCTTAGTTGAGAGCCCATGAAAAATC 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                          69
                                                                        65 GAACTTGTGTGTGCACCCTAATTATTGCTCAGATGTGGCAATGGAGCTTCTATATTA 124
                                                                                                                                   Local Similarity
                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                            IDENTIFICATION METHOD:
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: APPLICATION NUMBER:
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30, 5856138
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                                                                                                                   68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boston
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                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                    other nucleic acid, synthetic DNA
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                                                                                                                                                                                                                                                                                  double
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                                                                                                                                8.9%;
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                                                                                                                                Score 35.6; DB Pred. No. 0.036;
                                                                                                                   Mismatches
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                                                                                                                                            DB 2;
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                                                                                                                   Indels
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RESULT 7
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US-08-733-446-24
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TELEPHONE: (617)523-3400
TELEPAX: (617)523-6440
TELEPX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 base pairs
                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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PRIOR APPLICATION DATA:
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                                                                                                                                     124 TGGTTCCCAAAGACCACGTAAAAAGGAAGACAATGTCTTAGTTGAGAGCCATGAAAAATC 183
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                                                                                                                                                                                                64 GAAGITGCAGGATGTGCACAATTTTGTTGCTTAGGTGCCCCCATTGGCTCCTCGTGATGC 123
                                                                                                                                                                                                                                65 GAACTTGTGTGGCTCTGCACCCTAATTATTGCTCAGATGTGGCAATGGAGCTTCTATATTA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                TENGTH: 245 DELEMENTH: 245 DELEMENTH: Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: NEUNER, George REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/733,446 FILING DATE: 18-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/926,787
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                                                                                                                                                       AGCTTCGATGAGAAGAAGGAAAGGAGATCTCAAGGTCTTCACAGAGAGACCGAGGAAAACAA 184
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5856138
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VENTION: HUMAN PARATHYROID HORMONE MUTEINS
PRODUCTION THEREOF
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                            double
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55.78;
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Pred. No. 0.036;
0; Mismatches 54;
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                                                                                                                    RESULT 8
US-08-733-446-26
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                                                                                Sequence 26, Application US/08733446 Patent No. 5856138
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TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 247 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.9%;
Best Local Similarity 55.7%;
Matches 68; Conservative
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                GENERAL INFORMATION:
APPLICANT: FUKUDA,
TITLE OF INVENTION:
TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
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NUMBER OF SEQUENCES:
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TOPOLOGY: lir
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5. 5856138
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                                                 Tsunehiko
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                  PRODUCTION THEREOF
                                HUMAN PARATHYROID HORMONE MUTEINS AND
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Pred. No. 0.037;
0; Mismatches 54;
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US-08-733-446-27/c
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                                                                                                                                Sequence 27, Application US/08733446
Patent No. 5856138
GENERAL INFORMATION:
APPLICANT: FUKUDA, Tsunehiko
TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTEINS AND
TITLE OF INVENTION: PRODUCTION THEREOF
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TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
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REGISTRATION NUMBER: 2564
REFERENCE/DOCKET NUMBER: 420:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE,
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,446
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/402,970
APPLICATION NUMBER: US/08/402,970
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                                                                                                                   NUMBER OF SEQUENCES:
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                                  CITY:
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CITY: Boston
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COUNTRY:
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                                               130 Water Street
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Pred. No. 0.037;
0; Mismatches 54;
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                                                                                 BRONSTEIN,
                                                                                 ROBERTS
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Query Match
Best Local Similarity
Whes 68; Conserve
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US-08-733-446-28
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                                                                                                                                                                                                                                                               Patent NO. 58501001:
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TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN;
ADDRESSEE: CUSHMAN
CURRENT APPLICATION DATA:
                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 250 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
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NAME: NEUNER, George W
REGISTRATION NUMBER: 2691
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APPLICATION NUMBER:
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           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                 STREET: 130 v
CITY: Boston
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OPERATING SYSTEM:
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                                            COMPUTER:
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                                                                                                      COUNTRY:
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NO. 5856138
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EDNESS: double
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SYSTEM: PC-DOS/MS-DOS
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55.7%;
                                                                                                                                                                                                                             HUMAN PARATHYROID HORMONE MUTEINS AND PRODUCTION THEREOF
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                                                                                                                                                                                  DIKE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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              Version #1.25
                                                                                                                                                                                  BRONSTEIN, ROBERTS
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RESULT 11
US-08-689-190-1
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                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: FUKUDA, Y.
APPLICANT: OSHIKA, Y.
APPLICANT: YAMADA, T.
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08689190 Patent No. 5714349
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TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617)523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 AGCTTCGATGAGAAGGAAGGAGGGGAGATGTCAAGGTCTTCACAGAGACCGAGGAAAACAA 184
                               APPLICATION NUMBER: US/08/689,190 FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 GAACTTGTGTGGTCTGCACCCTAATTATTGCTCAGATGTGGCAATGGAGCTTCTATATTA 124
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                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/926,787
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                                                                                                                                                                               02109
                                                                                                                                                                                                                          Boston
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EDNESS: double
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                                                                                                                                                                                                           Massachusetts
                                                                                                                                                                                                                                           130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 base pairs
                                                                                                                                                                                                                                                                                                                                                       YAMADA, Takao
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                                                                                                                                                                                                                                                                       DAVID G. CONLIN;
                                                                                                                                                                                                                                                           CUSHMAN
                                                                                                                                            Floppy disk
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                                                                                                                                                                                                                                                                                                                      SYNTHETIC GENE CODING PARATHYROID HORMONE
                                                                                                                                                                                                                                                                                                                                                                                       Tsunehiko
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US/08/006,197
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                                                                                                                                                                                                                                                                         DIKE, BRONSTEIN, ROBERTS
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                                                                                                                                                                                                                                                                                                                                                             Sequence 23, Application US/08733446 Patent No. 5856138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.9%;
Best Local Similarity 55.7%;
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: 18-0CT-1996
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TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                COUNTRY: UZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
CLASSIFICATION:
                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                             STATE:
                                                                                                                                                                                           CITY: Boston
                                                                                                                                                                                                                           ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS ADDRESSEE: CUSHMAN
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APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                              130 Water Street
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                                                                                                                                                                                                                                                                                          HUMAN PARATHYROID HORMONE MUTEINS AND PRODUCTION THEREOF
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fOD: S
                              US/08/733,446
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US-08-733-446-56
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REFERENCE, DOCKET NUMBER: 4202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEFAX: (617)523-6440
TELEFX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 56, Appli
Patent No. 5856138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                            MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                             APPLICATION NUMBER: US/08/733,446 FILING DATE: 18-OCT-1996
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IDENTIFICATION METHOD:
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                 FILING DATE:
                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                 ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
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                                APPLICATION NUMBER:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                               130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                FUKUDA, Tsunehiko
VENTION: HUMAN PARATHYROID HORMONE MUTEINS
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                                                                                                                                                                                                                                                                                                                                                   62
US/07/926,787
                              US/08/402,970
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RESULT 14
US-08-733-446-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
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SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FUKUDA,
TITLE OF INVENTION:
TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN;
ATTORNEY/AGENT INFORMATION: NAME: NEUNER, George W
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                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                  APPLICATION NUMBER: US/08/733,446 FILING DATE: 18-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                  FILING DATE:
                                                    APPLICATION NUMBER: US/07/926,787
                                                                  FILING DATE:
                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                             ZIP: 02109
                                                                                                                                                                                                                                                                                                                           CITY: Boston
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VENTION: HUMAN PARATHYROID HORMONE MUTEINS AND

VENTION: PRODUCTION THEREOF
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                                                                                  US/08/402,970
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US-08-733-446-58
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TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5856138
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 58, Application US/08733446 Patent No. 5856138
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Best Local
                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,446
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                 FILING DATE:
APPLICATION NUMBER: US/07/926,787
FILING DATE:
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NAME/KEY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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          NAME: NEUNER, George W
REGISTRATION NUMBER: 20
                                                                                                                 APPLICATION NUMBER:
REFERENCE/DOCKET NUMBER:
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mutation
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42025
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; NAME/KEY: CDS
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US-08-733-446-58
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Best Local Similarity
"-+-hes 68; Conserva
Search completed: January Job time: 76 secs
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TELEPHONE: (617)523-3400
TELEPAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 58:
                                                              185 CC 186
| | |
198 CC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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                                                                                                                            138 TGGTTCCCAAAGACCACGTAAAAAGGAAGACAATGTCTTAGTTGAGAGCCATGAAAAATC 197
                                                                                                                                               125 AGCTTCGATGAGAAGGAAGGAAGGGGAGAGTCTAGAGGTCTTCACAGAGACCGAGGAAAACAA 184
                                                                                                                                                                                                               65 GAACTTGTGTGGGCGCCCCTAATTATTGCTCAGATGTGGGCAATGGAGCTTCTATATTA 124
                                                                                                                                                                                            78 GAAGTTGCAGGATGTGCACAATTTTGTTGCCTTAGGTGCCCCCATTGGCTCCTCGTGATGC 137
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Pred. No. 0.037;
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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Published_Applications_Na:*

1: /cgn2_6/ptodata/2/pubpna/U
2: /cgn2_6/ptodata/2/pubpna/U
3: /cgn2_6/ptodata/2/pubpna/U
4: /cgn2_6/ptodata/2/pubpna/U
5: /cgn2_6/ptodata/2/pubpna/U
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6: /cgn2_6/ptodata/2/pubpna/U
9: /cgn2_6/ptodata/2/pubpna/U
10: /cgn2_6/ptodata/2/pubpna/U
11: /cgn2_6/ptodata/2/pubpna/U
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13: /cgn2_6/ptodata/2/pubpna/U
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12: /cgn2_6/ptodata/2/pubpna/U
13: /cgn2_6/ptodata/2/pubpna/U
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_EWE_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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19	18	17	16	15	14	13	12	11	10	9	æ	7	6	Ç.	4	ω	2	1	No.	Result
31.2	31.2	31.2	31.2	31.2	31.2	31.2	31.6	32	32.2	32.2	32.2	32.2	32.2	32.2	33.4	34.8	34.8	36.4	Score	
7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.9	8.0	8.0	8.0	8.0	8.0	8.0	8.0	8.3	8.7	8.7	9.1	Match	Operv
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10	10	10	9	9	9	9	10	10	10	10	10	10	10	10	10	10	9	10	DB	
US-09-795-668-425	US-09-795-668-424	US-09-795-668-423	US-09-946-807-426	US-09-946-807-425	US-09-946-807-424	US-09-946-807-423	US-09-864-761-4541	US-09-835-232-6	US-09-815-242-8275	US-09-815-242-4500	US-09-764-847-1452	US-09-764-847-1451	US-09-764-847-1450	US-09-764-847-1449	US-09-070-927A-618	US-09-738-973-390	US-09-854-133-390	US-09-835-995-1	ID	
Sequence 425, App	Sequence 424, App	Sequence 423, App	Sequence 426, App	Sequence 425, App	Sequence 424, App	Sequence 423, App	Sequence 4541, Ap	Sequence 6, Appli	Sequence 8275, Ap	Sequence 4500, Ap	Sequence 1452, Ap	Sequence 1451, Ap	Sequence 1450, Ap	Sequence 1449, Ap	Sequence 618, App	Sequence 390, App	Sequence 390, App	Sequence 1, Appli	Description	

RESULT 2 US-09-854-133-390/c ; Sequence 390, Application US/09854133 ; Publication No. US20020183499A1

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45	44	43	42	41	40	39	38	37	36	35	34	$\omega$	32	31	30	29	28	27	26	25	24	23	22	21	
29.8	30	30.2	30.2	30.4	30.4	30.4	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.8	30.8	30.8	30.8	31	31	31.2	31.2	31.2	31.2	31.2	
7.4	7.5	7.5	7.5	7.6		7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.7	7.7	7.7	7.7	7.7	7.7	7.8	7.8	7.8	7.8	7.8	
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9	10	9	10	10	9	10	10	10	9	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	
US-09-938-842A-3362	US-09-895-828-286	US-09-938-842A-3151	US-09-960-352-7539	US-09-833-381-1015	US-10-153-273-7	US-09-983-965-3462		US-09-795-668-1	US-09-946-807-1	US-09-906-453-3	US-09-925-300-276	US-09-815-242-9010	US-09-815-242-8879	US-09-841-786-15	US-09-841-786-8	US-09-841-786-11	US-09-960-352-12123	US-09-973-451-38	US-09-983-965-4361	US-09-764-847-264	US-09-795-686-426	US-09-795-686-425	US-09-795-686-424	US-09-795-686-423	
Sequence 3362, Ap	Sequence 286, App	Sequence 3151, Ap	Sequence 7539, Ap	Sequence 1015, Ap	Sequence 7, Appli	Sequence 3462, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 276, App	Sequence 9010, Ap	Sequence 8879, Ap	Sequence 15, Appl	Sequence 8, Appli	Sequence 11, Appl	Sequence 12123, A	Sequence 38, Appl	Sequence 4361, Ap	Sequence 264, App			Sequence 424, App	Sequence 423, App	

### ALIGNMENTS

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2553
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-835-995-1
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US-09-835-995-1/c
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                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Soderberg, Charlotte
APPLICANT: Lind, Peter
TITLE OF INVENTION: NO. US20020052021A1e1 G Protein Coupled Receptors
FILE REFERENCE: 00146reg.US
CURRENT APPLICATION NUMBER: US/09/835,995
CURRENT FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 60/198,090
PRIOR FILING DATE: 2000-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                          151 ATGTCAAGGTCTTCACAGAGACCGAGGAAAACAACCAGATTCCAGGGCCAAGGGCTTGGA 210
708 TATGTAACACACTA 695
                                                                                                                     211 ATCCCATATTTCCTTTGACTTCAGGTGGACAATTTTAGAAGGCAATATTTAAATCTGGAA 270
                                                                                                                                                                              828 ATAACAAGCTCTGGAAGAGTACAGAAGAATGACTACAGAGCCCCACGACGACAGTCTGGCA 769
                                            271 GGGGTAAAGAACAA 284
                                                                                       768 CAGAGACATACCCTTTGATTCGAGGTAGACATTAGCTGATGACATTTTTGTAATTTTGCA 709
                                                                                                                                                                                                                                                                  9.1%; Score 36.4; DB 10; ilarity 54.5%; Pred. No. 0.15; Conservative 0; Mismatches 61;
                                                                                                                                                                                                                                                                       Indels
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GENERAL INFORMATION:

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                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-738-973-390
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                                                                                                                                                                                SOFTWARE: Fas:
SEQ ID NO 390
LENGTH: 1984
                                                                                                     Query Match
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 390
                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. US20020110563A1
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                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
                                                                                                                                                                                                                                                                             APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF
FILE REFERENCE: 210121.475C9
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C10
                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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CURRENT FILING DATE: 2001-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lodes, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1984
908 ATAACAAGCTCTGGAAGAGTACAGAAGAATGACTACAGAGCCCCACGATGACAGTCTGGCA 849
                              151 ATGTCAAGGTCTTCACAGAGACCGAGGGAAAACAACCAGATTCCAGGGCCAAGGGCTTGGA 210
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                                                                 Local Similarity
nes 72; Conserv
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                                                                                                                                                                                                                     FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                 Mannion, Jane
Kalos, Michael D.
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Elliot, Mark
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Benson, Darin R.
                                                                                                                                                                                                                                                                                                                                                                                                                   Algate, Paul A.
Secrist, Heather
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Lodes, Michael J.
Fling, Steven P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mohamath, Raodoh
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                                                                  Conservative
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                                                                                8.7%;
53.7%;
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53.7%;
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                                                               Score 34.8; DB Pred. No. 0.41; 0; Mismatches
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                                                                                                 DB 10;
                                                                 62;
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                                                                                                                                                                                                                                                                                                    LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1984;
                                                                 Indels
                                                                                                Length 1984;
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; Sequence 618, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
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RESULT 5
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                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 618: SEQUENCE CHARACTERISTICS:
                                                                                                                              655
                                                       595
                                                                          298 ATTGTGGAGGTTCAGATCATAAT 320
                                                                                                                                                 238 GACAATTTTAGAAGGCAATATTTAAATCTGGAAGGGGTAAAGAACAATCAGATGGTGTTA 297
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                                                                                                                                                                                                     Local Similarity
nes 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                            GAAAATATAAGGAGGCAATTTTTAATATTGCCAATGATAAATTACTTATAGCTTTTGGTA 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGAGACATACCCTTTGATTCGAGGTAGACATTAGCTGATGACATTTTTGTAATTTTTGCA 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGGTAAAGAACAA 284
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                                                                                                                                                                                                                                                                                                              LENGTH: 989 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/046,655 FILING DATE: 1997-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDRESSEE:
                                                                                                                                                                                                       Conservative
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62.7%;
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RESULT 7
US-09-764-847-1451
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; LENGTH: 642
; TYPE: DIA
; ORGANISM: Homo sapiens
US-09-764-847-1450
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US-09-764-847-1450
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1449
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GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
                                                                                                                    Sequence 1451, Application US/09764847 Patent No. US20020132767A1
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2003 SOFTWARE: Patentin Ver. 2.0
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Local Similarity 63.6%;
les 49; Conservative
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Local Similarity 63.6%;
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Pred. No. 1.5;
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; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1451
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US-09-764-847-1452
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SEQ ID NO 1451
LENGTH: 642
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               APPLICANT: Xu, H. Howard TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA. 011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
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TITLE OF INVENTION: Nuccleic Acids, Proteins, and Antibodies
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PRIOR APPLICATION NUMBER:
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TYPE: DNA
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nes 49; Conserv
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Local Similarity 63.6%;
es 49; Conservat:
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Yamamoto, Robert T.
Xu, H. Howard
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Zyskind, Judith W.
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Pred. No. 1
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APPLICATION NUMBER: 60/206,848 FILING DATE: 2000-05-23

FILING DATE:

2000-03-21

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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PRIOR DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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                                                                     PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA 011A
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                    SOFTWARE:
                                    NUMBER OF SEQ ID NOS:
                                                       PRIOR FILING DATE:
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NO 8275
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Yamamoto, Robert T.
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Zyskind, Judith W.
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                for Windows Version
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51.0%; Pred. No. 1
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US-09-815-242-8275
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                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                                        Matches
                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Leader, Benjamin
TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 00383/052002
                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/835,232 CURRENT FILING DATE: 2001-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Leder, Philip APPLICANT: Leader, Benji
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 22
                                                                                                                           22235
                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc_feature LOCATION: (1)...(18021)
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22355
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                             GGCAATATTTAAATCTGGAAGGGG 274
                                                                                                                           CTGATGCATTCCATTTCTGGTTTCTTTTG 354
TGTTTTCTTAAAACCAGGCTTGGG 22378
                                                             TCCATAAAGCATTGATTGTTACACAAATATGGTTCTCAGTTCTGTATGACAAATATAAAG 22354
                                                                                          TCCAGGGCCAAGGGCTTGGAATCCCATATTTCCTTTGACTTCAGGTGGACAATTTTAGAA 250
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Pred. No.
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Pred. No. 1.8;
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RESULT 12
US-09-864-761-4541
; Sequence 4541, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:

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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 49117
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1712 TTGAATTTTCTATTTAGTATATACATTTTTCTTCTTTTTGAAATGTGTATTTTCTAGT 1771
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HOMO SAPIENS

INFORMATION: MAP TO AC002094.1

INFORMATION: EXPRESSED IN PLACEN INFORMATION: EXPRESSED IN ADULT INFORMATION: EXPRESSED IN BT47/
R INFORMATION: EXPRESSED IN LUNCER INFORMATION: EXPRESSED IN BRAISER INFORMATION: EXPRESSED IN HE INFORMATION: EXPRESSED IN HE INFORMATION: EXPRESSED IN HE INFORMATION: EXPRESSED IN FUNCTIONAL EXPRESSED IN EXPRESSED EXPRESSED IN EXPRESSED                                                               207 TGGAATCCCATATTTCCTTTGACTTCAGGTGGACAATTTTAGAAGGCAATATTTAAAATCT 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00662
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38; Conservative
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                                                                                                                                     Score 31.6; DB Pred. No. 4.4; 0; Mismatches
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N BT4/4, SIGNAL = 31
N LUNG, SIGNAL = 1.5
N BRAIN, SIGNAL = 1.5
N HEART, SIGNAL = 1.9
N HELA, SIGNAL = 3.6
N HELA, SIGNAL = 3.6
N HELA, SIGNAL = 3.1
N HELLON, SIGNAL = 1.1
N FETAL LIVER, SIGNAL = 1.1
N FETAL LIVER, SIGNAL = 1.1
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US-09-946-807-424/c
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                                                                                                                                                                                                                                                                          Sequence 424, Application US/09946807 Patent No. US20020165144A1 GENERAL INFORMATION:
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Best Local
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SOFTWARE:
                                                    CURRENT APPLICATION NUMBER: US/09/946,807
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000-02-28
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TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
                                                                                                                                                                          APPLICANT: Steinthorsdottir, Valgerdur APPLICANT: Gulcher, Jeffrey Refreyer TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE FILE REFERENCE: 2345.2004-001
                                                                                                                                                                                                                APPLICANT: Stefansson, APPLICANT: Steinthors, APPLICANT: Gulcher, Ju
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                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US/09/795,668 PRIOR FILING DATE: 2001-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/946,807
CURRENT FILING DATE: 2001-09-05
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                       181 ACAAGTGAATTTGACAAAGCATTGTCTTTTTAATCATGGTAGTTTTCCTT 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 ARAAAATTGAGAGGCAGCTTCTAGTTCTTTCGGGCCCCTTCATTTCCTATTTCCCAAGGRA
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                  FastSEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Pred. No. 2.
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GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUWAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION HUWBER: US/09/946,807
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR APPLICATION NUMBER: US 09/515,716
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; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 425

; LENGTH: 401

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-946-807-425
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-946-807-424
Search completed: January 2, 2003, 15:06:42 Job time: 129 secs
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US-09-946-807-425/c
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Best Local Similarity 47.6%;
Matches 81; Conservative
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                                                                                                                               298 ATTGTGGAGGTTCAGATCATAATGCCATCTGATGCATTCCATTTCTGGTT 347
                                                                                                                                                                                                   199 AGCCAAGTTAAAGTGTCTACTCARAATGTGGCCGGCATTTWACACAATTAGATTGTGATA 140
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                                                                                                  ACAAGTGAATTTGACAAAGCATTGTCTTTTTAATCATGGTAGTTTTCCTT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
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Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd
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2687.392 Million cell updates/sec
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/cgn2_6/ptodata/1/pna/US6013_COMB.seq:
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/cgn2_6/ptodata/1/pna/US6001_COMB.seq
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

c 19 c 20 c 21	c 15 18	11 12 13	10	1 O U P W	Result NO. 1
220 220 220	221.4 221.4 220.6 220	255 255 223.6 223.4	266.8 264 264 264	402 402 266.8 266.8	Score 402 402
54.7 54.7 54.7	55.1 54.9 54.7	55.6 55.6	66.4 65.7	100.0 100.0 66.4 66.4	Query Match Length
484 545 550	1694 1694 570 484	385 385 1446 1444	433 433 433	402 402 426	uength [
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	Sequence 262628, Sequence 262628, Sequence 116358, Sequence 15731, A	Sequence 10, Appl Sequence 10, Appl Sequence 52180, A Sequence 50583, A	Sequence 451847, Sequence 451847, Sequence 1092, Ap Sequence 1089, Ap		Description Sequence 457554, Sequence 457554,

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RESULT 1

US-09-654-617-457554
Sequence 457554, Application US/09654617
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
INJUGUONG
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/654,617
CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 463173
SEQ ID NO 457554
LENGTH: 402
TYPE: DNA
ORGANISM: Sorghum bicolor
US-09-654-617-457554
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US-10-219-999-1814
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US-60-209-830-11200
US-60-209-4830-11458
US-09-865-439A-11458
US-10-219-999-22880
US-10-219-999-22880
US-10-219-999-20024
US-09-865-419A-42700
US-09-865-419A-42700
US-09-865-419A-43924
US-09-865-439A-18142
US-09-865-439A-18142
US-09-865-439A-18142
US-60-207-458-13361
US-09-865-439A-3361
US-09-865-439A-3361
US-09-865-439A-3361
US-09-865-439A-3361
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US-09-865-439A-33694
US-09-865-439A-33694
US-09-795-301-466
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Annotated Plant Genes
CURRENT APPLICATION NUMBER: US/09/684,016
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US/09/654,617
PRIOR FILING DATE: 2000-09-05
INUMBER OF SEQ ID NOS: 463173
SEQ ID NO 457554
CORGANISM: Sorghum bicolor
US-09-684-016-457554
APPLICANT: Andersen, Scott E.
APPLICANT: Andersen, Michael D
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: Nucleic Acid Molecules And
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51914)B
CURRENT APPLICATION NUMBER: US/09/850,147
CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: US 60/202,213
PRIOR APPLICATION NUMBER: US 60/202,213
PRIOR APPLICATION NUMBER: US 09/654,617
PRIOR FILING DATE: 2000-09-05
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US-09-684-016-457554
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; GENERAL INFORMATION:
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GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 402; Conservative 0;
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APPLICANT: Liu, Jingdong
TITLE OF INVENTION:
FILE REFERENCE: 38-2
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Pred. No. 1.3e-109;
Mismatches 0;
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APPLICANT: Andersen, Scott E.
APPLICANT: Edgerton, Michael D.
TITLE OF INVENTION: NUCLEIC ACID MOLECI
TITLE OF INVENTION: PLANTS
FILE REFERENCE: 38-21($1914)A
CURRENT APPLICATION NUMBER: US/60/202,213
CURRENT FILLNG DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 17986
SEQ ID NO 1
SEQ ID NOS: 17986
                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Sorghum bicolor
; OTHER INFORMATION: Clone ID: LIB3476-001-Q6-K1-A3
US-60-202-213-1
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; ORGANISM: Sorghum l
; OTHER INFORMATION:
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CCTTGAACTTGTGTGGTCTGCACCCTAATTATTGCTCAGATGTGGCAATGGAGCTTCTAT
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                                                                                                              Score 402; DB 64;
Pred. No. 1.3e-109;
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Pred. No. 1.3e-109;
Mismatches 0;
                                                                                                      Mismatches
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                                                                                                                             Length
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TYPE: DNA Sorghum bicolor OTHER INFORMATION: Clone ID: LIB3476-004-Q6-K1-A3 US-09-850-147-40
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Best Loc
Matches
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TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51914)B
CURRENT APPLICATION NUMBER: US/09/850,147
CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: US 60/202,213
PRIOR APPLICATION NUMBER: US 60/202,213
PRIOR FILING DATE: 2000-05-08
PRIOR FILING DATE: 2000-09-05
PRIOR FILING DATE: 2000-09-05
PRIOR FILING DATE: 2000-09-05
PRIOR FILING DATE: 2000-09-05
PRIOR FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 18014
SEQ ID NO 40
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Local Similarity
es 337; Conserv
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                                                                           ACAACCAGATTCCAGGGCCAAGGGCTTGGAATCCCATATTTCCTTTGACTTCAGGTGGAC
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                              AATTTTAGAAGGCAATATTTAAATCTGGAAGGGGTAAAGAACAATCAGATGGTGTTAATT
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Pred. No. 5.3e-69;
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US-09-654-617-451847
Sequence 451847, Application US/09654617
GENERAL INFORMATION:
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ORGANISM: Sorghum bicolor
OTHER INFORMATION: Clone
US-60-202-213-40
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       CURRENT APPLICATION NUMBER: US/09/654,617
CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 463173
SEQ ID NO 451847
LENGTH: 456
TYPE: ....
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38-21(51914)A
CURRENT APPLICATION NUMBER: U5/60/202,
CURRENT FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 17986
SEQ ID NO 40
LENGTH: 426
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                                                                                 APPLICANT: Liu, Jir
TITLE OF INVENTION:
FILE REFERENCE:
                                                                                                                            APPLICANT:
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APPLICANT: Edgerton, Michael
TITLE OF INVENTION: NUC
TITLE OF INVENTION: PLANTS
  TYPE: DNA
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SEQ ID NO 451847
LENGTH: 456
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                            CCTTGTAACTGTGGTGCTGCACCTAATTATTGCTACAGATGTGGCAATGTAGCTTCTAT 143
ATTAAGCTTCGATGAGAAGGAAGGAAGGAGGTCTCAAGGTCTTCACAGAGACCGAGGAAA 180
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; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(456)
; OTHER INFORMATION: unsure at all n locations
US-09-684-016-451847
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; OTHER INFORMATION: unsure at all n locations
US-09-654-617-451847
                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/684,016
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/654,
PRIOR FILING DATE: 2000-00-00
NUMBER OF CONTROL OF THE PRIOR FILING DATE: 2000-00-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AATTTTAGAAGGCAATATTTAAATCTGGAAGGGGTAAAGAACAATCAGATGGTGTTAATT 300
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CCCGGGCGGCTCACCAGCTGGTCCAGGAAGGCTTAAAGTACATGTTCCAGGAGAA-GGG 83
                                          CCGGGCCGGGCTCACCAGCTGGCCCCAGTGAAGGCCTTAAAGACATGTGCCAGGAGAAGGGG 60
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SEQ ID NO 1092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Andersen, Scott E.
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51914)B
CURRENT APPLICATION NUMBER: US/09/850,147
CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: US 60/202,213
PRIOR FILING DATE: 2000-05-08
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 09/654,617
PRIOR APPLICATION NUMBER: US 09/654,617
PRIOR APPLICATION NUMBER: US 09/664,016
PRIOR FILING DATE: 2000-09-05
PRIOR FILING DATE: 2000-10-10
                                                                                                                                                                                                                                                                                                                                              NAME/KRY: unsure
LOCATION: (1)..(433)
OTHER INFORMATION: unsure at
OTHER INFORMATION: Clone ID:
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Sorghum
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                                                     AGATTCCAGGGCCAAGGGCTTGGAATCCCATATTTCCTTTGACTTCAGGTGGACAATTTT
                                                                                                           TGTACAATAGACCATCGGGAGTGTCATATCTTCCTGTATTCC
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                  AGAAGGCAATATTTAAATCTGGAAGGGGTAAAGAACAATCAGATGGTGTTAATTGTGGAG
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84.1%;
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LIB3476-004-Q6-K2-A3
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Pred. No. 3.7e-68;
0; Mismatches 60;
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TYPE: DNA
CORGANISM: Sorghum b
COTHER INFORMATION:
US-60-202-213-1089
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US-60-202-213-1089
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CURRENT APPLICATION NUMBER: US/50/202,213
CURRENT FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 17986
SEQ ID NO 1089
LENGTH: 433
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TITLE OF INVENTION: NUCLEI
TITLE OF INVENTION: PLANTS
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          AAAAACCAACGGGAGGGGCATAACTTCCTGTGTTCC
                                                       GTTCAGATCATAATGCCATCTGATGCATTCCATTTCTGGTTTTCTTTTGAACACAAGTACA
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                                           ACTTGTGTGGTCTGCACCCTAATTATTGCTCAGATGTGGCAATGGAGCTTCTATATTAAG
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84.1%;
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Pred. No. 3.7e-68;
0; Mismatches 60
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APPLICANT: Andersen, Scott E.
APPLICANT: Andersen, Michael D
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: Nucleic Acid Molecules /
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51914)B
CURRENT APPLICATION NUMBER: US/09/850,147
CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: US 60/202,213

Molecules

And

Other

Molecules

Associated

With

US-09-850-147-10

Sequence 10, Application US/09850147 GENERAL INFORMATION:

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NUCLEIC ACID MOLE
LLE REFERENCE:
38-21(51914)A
CURRENT APPLICATION NUMBER: US/60/202,213
CURRENT FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS:
SEQ ID NO 10
LENGTON
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                                                                                                                    ; LENGTH: 385
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; OTHER INFORMATION: Clone:
US-60-202-213-10
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US-60-202-213-10
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; ORGANISM: Sorghum bicolor
; OTHER INFORMATION: Clone ID: LIB3476-001-Q6-K2-A3
US-09-850-147-10
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Best Local S
Matches 324
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APPLICANT: Edgerton,
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE:
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PRIOR APPLICATION NUMBER: US 09/684,016
PRIOR FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 18014
SEQ ID NO 10
LENGTH: 385
                                                                                Query Match
Best Local :
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APPLICATION NUMBER: US (
FILING DATE: 2000-09-05
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                                                                    Conservative
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                                                                              63.4%;
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                                                                  Score 255; DB 64;
Pred. No. 1.8e-65;
0; Mismatches 60;
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Pred. No. 1.8e-65;
D; Mismatches 60;
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; NAME/KEY: misc_feature
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US-09-708-427-52180
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SEQ ID NO 52180
LENGTH: 1446
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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                     TTTAGAAGGCAATATTTAAATCTGGAAGGGGTAAAGAACAATCAGATGGTGTTAATTGTG
                                                         ACCAGATTCCAGGGCCAAGGGCTTGGAATCCCCATATTTCCTTTGACTTCAGGTGGACAAT
                                                                                         AAGCTTCGATGAGAAGATGGAAAGG-GATGTCAAGTTCTTCACAGAGACAGAGGAGAACA 1183
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; Sequence 50583, Application US/09513996A
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA E
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-709P
; CURRENT APPLICATION NUMBER: US/09/513,996A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 81028
                                                                          RESULT 15
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                                             Sequence 262628, Application US/09654617 GENERAL INFORMATION:
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APPLICANT: KO
APPLICANT: Liu, Ji
TITLE OF INVENTION:
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                                                                                                                                          CAATAGACCATCGGGACAGTCATATGTTCCTGTAT 1394
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SEQ ID NO 262628
LENGTH: 1694
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                                                                                                                        TTAGAAGGCAATATTTAAATCTGGAAGGGGTAAAGAACAATCAGATGGTGTTAATTGTGG 304
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ACAATAGACCATCCGGACAGTCTCATGCTCCTGTATCCC 1374
                           ACAAAAACCAACGGGAGGGGCATAACTTCCTGTGTTCC 402
                                                          AGGTCCAGATCATAGTGCAATCTGATGCGTTTGATTTCTCTTTTTCCTTTTAACCACATGT
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78.7%;
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Search completed: January 2, 2003, 14:25:02 Job time: 3766 secs



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Result
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1: /cgn2_6/ptodata/1/pna/P

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4: /cgn2_6/ptodata/1/pna/U

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/cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
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PCT-US02-28445-13
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US-09-724-676A-16911
US-09-724-676A-16914
US-09-724-676A-16912
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US-09-724-676A-16912
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US-09-724-676A-16915
US-09-724-676A-16915
US-09-724-676A-16915
US-09-724-676A-16910
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US-09-724-676A-169013
US-09-724-676A-16905
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Sequence 5, App.
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<ul> <li>Sequence 1</li> </ul>	Sequence 1	Sequence 1	Sequence 1	sequence I														
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## ALIGNMENTS

RESULT 1 US-09-531-113-41876/c ; Sequence 41876, Application US/09531113

GENERAL INFORMATION:

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APPLICANT: Byrum, Joseph R.
APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15761)B
CURRENT APPLICATION NUMBER: US/09/531,113
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 48629
SEQ ID NO 41876
LENGTH: 533
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: JC-gmro02910026c05a1
US-09-531-113-41876
RESULT 2
PCT-US02-28445-13
Sequence 13, Application PC/TUS0228445
GENERAL INFORMATION:
APPLICANT: BASE PLANT SCIENCE GMBH
TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEPTIDES
TITLE OF INVENTION: METHODS OF USE IN PLANTS
FILE REFERENCE: 16313-0160
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nilarity 69.8%;
Conservative
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Pred. No. 4.2e-17;
0; Mismatches 67;
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CURRENT FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: 60/317,305
PRIOR FILING DATE: 2001-09-05
NUMBER OF SEO ID NOS: 43
SOFTWARE: Patentin Ver. 2.1
SEO ID NO 13
LENGTH: 1184
                                                                                                                                        Best Local Similarity Matches 172; Conserv
                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                 SEQ ID NO 13
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Best Local
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CURRENT FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: 60/317,305
                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEPTIDES TITLE OF INVENTION: METHODS OF USE IN PLANTS FILE REFERENCE: 16313-0161
                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-09-05
NUMBER OF SEQ ID NOS: 43
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ORGANISM: Glycine
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GTAACTGTATGGTCTGCACCTAATTACTGTTACCGATGTGGAAATGTAGCTTCTATTCTG 906
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COSTA E SILVA, OSWALDO DA
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Pred. No. 9.1e-17;
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RESULT 5
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; SEQ ID NO 2951
; LENGTH: 539
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER IMFORMATION: Clone ID: jC-gmf102220053a07d1
US-09-531-113-2951
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                                                                                                     Sequence 5, Application PC/TUS0228445

GENERAL INFORMATION:
APPLICANT: BASE PLANT SCIENCE GMBH
TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEPTIDES AND
TITLE OF INVENTION: METHODS OF USE IN PLANTS
FILE REFERENCE: 16313-0160
CURRENT APPLICATION NUMBER: PCT/US02/28445
CURRENT FILING DATE: 2002-09-05
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GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: Heck, Gregory I
SOFTWARE:
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Best Local Similarity
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APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules And
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15761)B
                                                               PRIOR APPLICATION NUMBER: 60/317,305 PRIOR FILING DATE: 2001-09-05
                                        NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/531,113
CURRENT FILING DATE: 2000-03-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAGATTCCAGGGCCAAGGGCTTGGAATCCCATATTTCCTTTGACTTCAGGTGGACAATT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTTGAATTTATTGTAAAAT 1044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCTTCGATGAGAAGAAGGAAGGAGATGTCAAGGTCTTCACAGAGACCGAGGAAAACAA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164;
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                      PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Pred. No. 3.9e-16;
0; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94;
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LENGTH: 1014

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TYPE: DNA
; ORGANISM: Physcomitrella patens
US-10-236-699-5
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; ORGANISM: Physcomitrella patens
PCT-US02-28445-5
RESULT 7
US-10-092-411A-981/c
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Best Local Similarity 61...
130; Conservative
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TITLE OF INVENTION: PROTEIN PHOSPHAFASE STRESS-RELATED POLYPEPTIDES AND
TITLE OF INVENTION: METHODS OF USE IN PLANTS
FILE REFERENCE: 16313-0161
CURRENT APPLICATION NUMBER: US/10/236,699
CURRENT FILING DATE: 2002-09-05
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/317,305
PRIOR EILING DATE: 2001-09-05
NUMBER OF SEQ ID NOS: 43
SOPTUBARE: TITLE DATE: 2001-09-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     789 GTCACGGTGTGGTCCGCTCCAAACTATTGCTACAGATGTGGAAATGTTGCTTCAATCTTA
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                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                          5 GCCGGGCTCACCAGCTGGCCCAGTGAAGGCTTAAAGACATGTGCCAGGAGAAGGGGCCTT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 GCCGGGCTCACCAGCTGGCCCAGTGAAGGCTTAAAGACATGTGCCAGGAGAAGGGGCCTT 64
                                                                        GGCTATGATGGCACCTCGAGCAGGAGTTCC 937
                                                                                                          CCAGATTCCAGGGCCAAGGGCTTGGAATCC 214
                                                                                                                                                                                                                   GTCACGGTGTGGTCCGCTCCAAACTATTGCTACAGATGTGGGAAATGTTGCTTCAATCTTA
                                                                                                                                                                                                                                                     GAACTTGTGTGGGCTCTGCACCCTAATTATTGCTCAGATGTGGCAATGGAGCTTCTATATTA 124
                                                                                                                                                                                                                                                                                         GCCGTGCGCATCAATTAGTTCAAGAGGGATTGAAGTACATGTTTCCTGACAA-AGGACTT 788
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                                                                                                                                              AGCTTCAACGAAAATATGGAGA-GAGATGTGAAATTTTTTACTGAGACCGAGGAGAACCA
                                                                                                                                                                             AGCTTCGATGAGAAGAAGGAAAGGAGATGTCAAGGTCTTCACAGAGACCGAGGAAAACAA 184
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ISHITANI, MANABU
                                                                                                                                                                                                                                                                                                                                                                  Conservative
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61.9%;
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61.9%;
                                                                                                                                                                                                                                                                                                                                                              Score 61.2; DB 6;
Pred. No. 9.6e-09;
0; Mismatches 78;
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Pred. No. 9.6e-09;
0; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                Length 1014;
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US-09-724-676-16911/c : Sequence 16911, Application US/09724676 ; GENERAL INFORMATION:
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SEQ ID NO 16911
LENGTH: 1291
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5676
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PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/092,411A CURRENT FILING DATE: 2002-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 032796-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lynn Doucette-Stamm et al
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NAME/KEY: misc_feature
LOCATION: (56)..(56)
OTHER INFORMATION: n is a,c,g,
                                                                           NAME/KEY: misc_feature
LOCATION: (51)..(51)
OTHER INFORMATION: n is
                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (46)..(46)
OTHER INFORMATION: n is
                                                                                                                                                                                                                                   LOCATION: (41)..(41)
OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: n is a,c,g,
                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature LOCATION: (31)..(31)
                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
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                                                              FEATURE:
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Pred. No. 1;
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (60)..(60)
; OTHER INFORMATION: n is
US-09-724-676-16911
δõ
                                                                                        ; LOCATION: (60)...(60)
; OTHER INFORMATION: n is a,c,g,
US-09-724-676A-16911
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                                                         Query Match
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Best Local (
                               Matches
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
                                                                                                                                                               LOCATION: (56)..(56)
OTHER INFORMATION: n is
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NAME/KEY: misc_feature
LOCATION: (31)...(31)
OTHER INFORMATION: n is
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                                                                                                                                   NAME/KEY: misc_feature
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OTHER INFORMATION: n is
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 254 AATATTTAAATCTGGAAGGGGTAAAGAACAATCAGATGGTGTTAATTGTGGAGGTTCAGA 313
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Local Similarity 52.58;
les 74; Conservation
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LENGTH: 1317
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CURRENT FILING DATE: 2000-11-28
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SOFTWARE: PatentIn version 3.2
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TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SED ID NOS: 97222
COMMERCE SED ID NOS: 97222
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 16912
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CURRENT FILING DATE: 2000-11-28
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US-09-724-676-16915/c; Sequence 16915, Application US/09724676
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Sequence TOTAL Sequence TOTAL Sequence TOTAL Sequence TOTAL APPLICANT: Compugen LTD APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative splicing; FILE REFERENCE: 129181.4 Compugen; FILE APPLICATION NUMBER: US/09/724,676
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SEQ ID NO 16912
LENGTH: 1358
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 16915
LENGTH: 1384
TYPE: DNA
TYPE: DNA
TYPE: DNA
TERRATISM: Homo sapiens
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US-09-724-676A-16915/c
Sequence 16915, Application US/09724676A
GENERAL INFORMATION:
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APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of FILE REFERENCE: 129181.4 Compuge
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 16915
LENGTH: 1384
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

62.8 493 12 BG558648	66.2 681 13 BG946826	66.2 614 10 BE597103	66.2 612 10 AW745589	66.2 606 14 BQ656076	568 10 AW565695 . AW565695	Result Query No. Score Match Length DB ID Description
BG558648 RHIZ2_58_	346826 IP1_1_B10	597103 PI1_70_G0	745589 WS1_35_A0	556076 pRC0407 S	565695 LG1_348_A	escription

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BQ120114 EST605690	CATTOO	TO FOR	•	<u>4</u>	34 AL50063	7 AV94609	249 HV04N10	756 вJ32275	10000	86368 вJ48636	AL4999	614045	8 614045H	HV041	AJ435241 AJ435241	вJ211965 вJ211965	вJ482869 вJ482869	AV943812 AV943812	AI619388 486093F06	ВJ466432 ВJ466432	AU031687 AU031687	AW679158 WS1_22_A0	вJ251011 вJ251011	A1902083 614022D04	вJ284678 вJ284678	BE598350 PI1_81_E1	BG354266 947033G03	~	•	MEST39-	79618 MEST97-B	24010 WS1_32	90 606022D02	288508 618068C	43 486090DO	57	_	AI978092 614022D04	AW091358 614094A10

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## ALIGNMENTS

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	TITLE JOURNAL COMMENT	ORGANISM REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 AW565695 LOCUS DEFINITION
The University of Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 583 0210 Email: mmprattGuga.edu Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20 Seq primer: T7 High quality sequence start: 29	An EST database from Sorghum: light-grown seedlings Unpublished (2000) Contact: Cordonnier-Pratt MM	Sorghum bicolor  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  clade; Panicoideae; Andropogoneae; Sorghum.  1 (bases 1 to 568)  Cordonniar-Pratt M -M Gingle A Marsala C and Bratt L H	sequence. AW565695 AW565695.1 GI:7219573 EST. sorghum.	AW565695 568 bp mRNA linear EST 19-JUL-2000 LG1_348_A05.g1_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA

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RESULT 2
BQ656076
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BRC0407 Sorghum halepense richna clone pRC0407, mRNA se BQ656076.1 GI:21788402
                                                                                                                                                                                                                                                                                                                            CAATAGACCATCGGGAGTGTCATATCTTCCTGTATTCC 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 335;
                                                                      Unpublished, Paterson, A. H
Unpublished (2002)
Contact: Paterson AH
          Riverbend Research Laboratory, GA 30602, USA Tel: 7065830162
                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.

1 (bases 1 to 606)
                                             Center for Applied Genetic Technologies University of Georgia
                                                                                                            Paterson, A.H.
                                                                                                                                                                         Sorghum halepense
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POLYA=Yes.
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/note="organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: XhoI, Site_2: Eco
; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."

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/db_xref="taxon:4558"
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Pred. No. 6.2e-71;
0; Mismatches 60;
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Plant Sca.
 Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
                                                                                                                                                                                                                                                                                                                                    AW745589 612 bp WS1_35_A09.g1_A002 Water-stressed mRNA_sequence.
                                                                                           An EST database from Sorghum: water-stressed Unpublished (2000)
                                                                                                                                                   Cordonnier-Pratt, M.-M., Gingle, A.,
                                                                                                                                                                    clade; Panicoideae; Andropogoneae;
1 (bases 1 to 612)
                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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/clone="pRC0407"
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/note="Vector: pBluescript SK(-);
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Pred. No. 6.3e-71;
0; Mismatches 60;
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                                                                                                                                                     Marsala,C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                      BE597103 614 PII_70_G02.g1_A002 Pathogen mRNA sequence.
Unpublished (2000)
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                                                    Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M.
                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.
                                                                                                                                                                                    EST
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Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                               Sorghum bicolor
                                                                                                                                                                                                  BE597103.1 GI:9852288
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                                                                         (bases 1 to 614)
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/note="Organ: Mix of 5-week old plants on days 7 & 8 after
water was withheld; Vector: Lambda Zap; Site_1: XhoI;
Site_2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
110 c 148 g 198 t
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/db_xref="taxon:4558"
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Pred. No. 6.3e-71;
0; Mismatches 60;
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  CAATAGACCATCGGGAGTGTCATATCTTCCTGTATTCC
                                                                                                              AGGTTCAGATCATAATGCCATCTGATGCATTCCATTTTCTGGTTTTCTTTTGAACACAAGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: PolyTMix
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     two-week-old sorghum plants 48 hr after inoculation;
two-week-old sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda Zap II; Site_1: xhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (Isolate FRM421 of
Colletotrichum graminicola, which is a Sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptiblity
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequenced were prepared by mass excision. WARNING: Whomost or all ESTs are expected to derive from the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4558"
/clone_lib="Pathogen induced 1 (PI1)"
/note="Organ: Anthracnose-infected leaves from
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84.2%;
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Pred. No. 6.4e-71;
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JOURNAL
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IP1_1_B10.g1_A002 I
mRNA sequence.
BG946826
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Sequences have been trimmed to exclude PolyA,
below Phred quality 16. The threshold for high
20. Three-prime sequences, which are obtained
sequencing primer, are presented as the revers
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Plant Sciences Building, Rm. 2502, Athens, GA 3 Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An EST database from Sorghum: 
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Cordonnier-Pratt MM
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Klein,R.R., Cordonnier-Pratt,M.-M., Gingle,A.,
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/note="Organ: Developing preanthesis pannicles; Vector:
/note="Organ: Developing preanthesis pannicles; Vector:
pBluescript II SK(-) from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
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/cultivar="BTx623"
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Seq primer: T7
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Fax: 706 583 0210
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
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Contact: Cordonnier-Pratt MM
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/note="Organ: Rhizomes; Vector: pBluescript II from Lamb
Znp II; Site_1: XhoI; Site_2: EcoRI; The library was mad
from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
90 c 115 g 157 t
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/db_xref="taxon:132711"
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855 California Ave,
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Contact: Walbot V
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614094 row: A column:
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/clone_lib="614 - root cDNA library from Walbot Lab"
/tissue_type="root"
/dev_stage="3-4 days old"
/lab_host="XLOLR"
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                                                                                                                                                  GAACTTGTGTGGTCTGCACCCTAATTATTGCTCAGATGTGGCAATGGAGCTTCTATATTA 124
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/lab_host="XLOLR"
/note="Organ: root; Vecto
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/clone_lib="614 - roo
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                                                CCAGATGCGAGGCCCAAGGAC-TGCAGTCCCATATTTCCTCTGACTTCAATTGTAC-ATT
                                                                                                   AGCTTCGATGAGAAGATGGAAA - GAGATGTCAAGTTCTTCACAGAGACAGAGAAAAACAA
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Plate: 614022 row: D column:
Location/Qualifiers
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Tel: 650 723 2227
Fax: 650 725 8221
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Contact: Walbot V
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EcoRI; Site_2: XhoI; 3-4 days old root tissue from
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                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="root"
/dev_stage="3-4 days old"
/lab_host="XLOLR"
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/clone_lib="614 - root cDNA library from Walbot Lab"
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/cultivar="W23"
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Submitted (25-APR-2002) Maize Mapping
Missouri, Columbia, MO 65211, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coe, E.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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314 c 286 g 310 t 89 others
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/db_xref="MaizeDB:630146"
/db_xref="taxon:4577"
/clone="CL12356_1"
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                                                                  CCAGATTCCAGGGCCAAGGGCTTGGAATCCCATATTTCCTTTGACTTCAGGTGGACAATT
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313; Conserv
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Plate: 486090 row: D column:
Location/Qualifiers
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855 California Ave, Palo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Walbot V
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1 (bases 1 to 470)
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a 109 c
                                                                                                                                                                                                                                                                                                                                               /tissue_type="leaf primordia"
/dev_stage="p7-p11 leaf"
/lab_host="0.col1 XL1-Blue_MFR'"
/note="Organ: shoot; Vector: Lamb
                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Zea mays"
/cultivar="B73" mays"
/db_xref="taxon:4577"
/clone_lib="486 - leaf primordia
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Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 590)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: walbot@stanford.edu
Plate: 618068 row: C col
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Tel: 650 723 2227
Fax: 650 725 8221
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Contact: Walbot V
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Inbred tassel library from Sc)
1 138 c 112 g 157 t
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/clone_lib="618 · Inbred Tassel cDNA Library"
/tissue_type="tassel"
/dev_stage="tassel length from 0.1 to 2.5 cm"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="2ea mays"
/cultivar="0hio43"
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 CCAGATGCGAGGCCCAAGGAC - TGCAGTCCCATATTTCCTCTGACTTCAATTGTAC - ATT
                                                              AGCTTCGATGAGAAGGAAGGAGAGGTGTCAAGGTCTTCACAGAGACCGGAGAAACAA 184
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                                                  AGCTTCGATGAGAAGATGGAAA-GAGATGTCAAGTTCTTCACAGAGACAGAGGAAAACAA
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 650 723 2227 Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Biological Sciences Stanford University
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Location/Qualifiers
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/cultivar="Ohio43"
/db_xref="taxon:4577"
/clone_lib="606 - Ear t
                                                                                                                                                                                                                                                                                             /dev_stage="ear length from 0.5 cm - 2.0 cm"
/lab_host="xLOLR (Stratagene)"
/note="Organ: immature ear; Vector: pBK-CMV; Site_1: EcoRI
; Site_2: XhoI; Mixed ear tissue cDNA library from Schmidt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, Tel: 706 542 1860
Fax: 706 583 0210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: numpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Cordonnier-Pratt MM
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1 (bases 1 to 413)
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An EST database from Sorghum: water-stressed
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                                                                                                                                                                                                                                                                                           /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Water-stressed 1 (WS1)"
/clone_lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after water was withheld; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."
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Pred. No. 3.6e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (<a href="http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b rt). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<a href="http://www.tigr.org/softlab/">http://www.tigr.org/softlab/</a>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve
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G405 Agronomy, Iowa State University, Ames, IA 50011-1010, US
Tel: 515-294-0975
Fax: 515-294-299
Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using
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/note="Vector: pT/T3PAC; Site_1: EcoRI; Site_2: NotI; /note="Vector: pT/T3PAC; Site_1: EcoRI; Site_2: NotI; /note="Vector: pT/T3PAC; Site_1: EcoRI; Site_2: NotI; /note="Vector: pT/T3PAC; Site_1: NotI /note="Vector: pT/T3PAC /note="Vector: note; pT/T3PAC /note="Vector: p
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/cultivar="B73"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Seedling and silk"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="MEST97-B02"
/clone_lib="ISUM4-TN"
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                             ACAAAAACCAACGGGAGGGGCATAACTTCCTGTGT 399
                                                                                                                                          TTAGAAGGCAATATTTAAATCTGGAAGGGGTAAAGAACAATCAGATGGTGTTAATTGTGG 304
                                                                                                                                                                                      CCAGATGCGAGGCCCAAGGAC-CGCAGTCCCATATTTCCTATGACTTCAATTGTACAATT
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                                                                                                                                                                                                                                                                                                                                   GAACTTGTGTGGTCTGCACCCTAATTATTGCTCAGATGTGGCAATGGAGCTTCTATATTA 124
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ACAATAGACCATCGGGACAGTCATATGTTCCTGTAT
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